

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2003, 20:56:26 ; Search time 86 Seconds (without alignment)

Title: US-09-383-579C-9
Perfect score: 992

Sequence: 1 gaataatcaacaacattgc.....aacacaacgcggaacgac 992

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database : Issued Patents NA: *

1:	/cgn2_6/ptodata/2/1na/5A_COMB.seq: *
2:	/cgn2_6/ptodata/2/1na/5B_COMB.seq: *
3:	/cgn2_6/ptodata/2/1na/6A_COMB.seq: *
4:	/cgn2_6/ptodata/2/1na/6B_COMB.seq: *
5:	/cgn2_6/ptodata/2/1na/PCTUS_COMB.seq: *
6:	/cgn2_6/ptodata/2/1na/backfiles1.seq: *

using seeds to improve read quality

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	681	68.6	681	2	US-08-440-517A-1	Sequence 1, Appli
2	681	68.6	681	3	US-09-092-160-1	Sequence 1, Appli
3	276.4	27.9	537	2	US-08-845-539-5	Sequence 5, Appli
4	276.4	27.9	537	4	US-09-362-642-5	Sequence 5, Appli
5	262.6	26.5	727	1	US-07-885-970A-6	Sequence 6, Appli
6	262.6	26.5	727	1	US-08-298-687A-6	Sequence 6, Appli
7	262.6	26.5	727	1	US-08-530-797-5	Sequence 5, Appli
8	262.6	26.5	727	1	US-08-298-829-6	Sequence 5, Appli
9	262.6	26.5	727	2	US-08-787-335-5	Sequence 6, Appli
10	256.6	25.9	2415	1	US-07-885-970A-26	Sequence 26, Appli
11	256.6	25.9	2415	1	US-08-298-687A-26	Sequence 26, Appli
12	256.6	25.9	2415	1	US-08-298-829-26	Sequence 26, Appli
13	251.6	25.4	702	2	US-08-845-539-1	Sequence 1, Appli
14	251.6	25.4	702	4	US-09-362-642-1	Sequence 1, Appli
15	242.8	24.5	501	2	US-08-845-539-3	Sequence 3, Appli
16	242.8	24.5	501	4	US-09-362-642-3	Sequence 3, Appli
17	92	9.3	279	4	US-09-313-294A-1276	Sequence 1276, Ap
18	68	6.9	7218	1	US-08-232-463-14	Sequence 14, Appli
19	46.6	4.7	2614	4	US-09-004-056-1	Sequence 1, Appli
20	46.2	4.7	4177	3	US-09-023-082A-23	Sequence 23, Appli
21	40.2	4.1	289	3	US-09-007-005-17	Sequence 17, Appli
22	40.2	4.1	289	3	US-09-244-796-17	Sequence 17, Appli
23	38.6	3.9	53526	3	US-08-658-136-2	Sequence 2, Appli
24	38.6	3.9	53577	3	US-08-658-136-1	Sequence 1, Appli
25	38	3.8	20966	4	US-09-984-880-3	Sequence 3, Appli
26	37.6	3.8	1664976	4	US-08-916-421B-1	Sequence 1, Appli
27	37.4	3.8	248	3	US-09-007-005-32	Sequence 32, Appli

C	28	37.4	3.8	248	3	US-09-244-796-32	Sequence 32, Appl
C	29	37.4	3.8	277	3	US-09-007-005-3	Sequence 3, Appli
C	30	37.4	3.8	277	3	US-09-244-796-3	Sequence 3, Appli
C	31	37.4	3.8	99500	4	US-09-798-096-10	Sequence 10, Appl
C	32	37	3.7	580073	4	US-08-545-528D-1	Sequence 1, Appli
C	33	36.8	3.7	1305	4	US-09-516-143A-1	Sequence 1, Appli
C	34	36.8	3.7	246240	2	US-08-724-394A-20	Sequence 20, Appl
C	35	36.8	3.7	246240	2	US-08-724-394A-21	Sequence 21, Appl
C	36	36.8	3.7	246240	2	US-08-724-394A-22	Sequence 22, Appl
C	37	36.6	3.7	5852	1	US-07-867-106-2	Sequence 2, Appli
C	38	36.2	3.6	1762	3	US-08-851-843A-3	Sequence 3, Appli
C	39	36.2	3.6	1762	3	US-08-974-549A-115	Sequence 115, App
C	40	36.2	3.6	1762	3	US-08-854-050-3	Sequence 3, Appli
C	41	36.2	3.6	1762	4	US-09-430-323-3	Sequence 3, Appli
C	42	36.2	3.6	72604	4	US-09-268-992-7	Sequence 7, Appli
C	43	36.2	3.6	72604	4	US-09-657-474-7	Sequence 7, Appli
C	44	36	3.6	152331	3	US-09-128-155-16	Sequence 16, Appl
C	45	36	3.6	176373	3	US-09-128-155-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-440-517A-1
; Sequence 1, Application US/08440517A
; Patent No. 5959082
; GENERAL INFORMATION.

✓
2/28/99 (E)? looked at all those

1 APPLICANT: COSGROVE, DANIEL J.;
 2 APPLICANT: GUILTINAN, MARK;
 3 APPLICANT: SHCHERBAN, TATYANA;
 4 APPLICANT: SHI, JUN
 5 TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
 6 NUMBER OF SEQUENCES: 6
 7 CORRESPONDENCE ADDRESSES:
 8 ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
 9 ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
 10 STREET: 113 TECHNOLOGY CENTER
 11 CITY: UNIVERSITY PARK
 12 STATE: PENNSYLVANIA
 13 COUNTRY: UNITED STATES OF AMERICA
 14 ZIP: 16802-7000
 15 COMPUTER READABLE FORM:
 16 MEDIUM TYPE: FLOPPY DISK
 17 COMPUTER: NEC 286
 18 OPERATING SYSTEM: DOS
 19 SOFTWARE: WORDPERFECT 5.1
 20 CURRENT APPLICATION DATA:
 21 APPLICATION NUMBER: US/08/440,517A
 22 FILING DATE:
 23 CLASSIFICATION: 530
 24 INFORMATION FOR SEQ ID NO: 1:
 25 SEQUENCE CHARACTERISTICS:
 26 LENGTH: 681
 27 TYPE: NUCLEIC ACID
 28 STRANDEDNESS: SINGLE
 29 TOPOLOGY: UNKNOWN

Query Match	68.6%	Score 681	DB 2	Length 681
Best Local Similarity	100.0%	Pred. No.	2e-197	
Matches 681; Conservative	0	Mismatches	0	Indels 0; Gaps 0

QY	223	GACTACGGTGGCTGGCAGAGCGGCCACGCCACCTTTATGTGTGTGATCCGATCTGGC	282
Db	1	GACTACGGTGGCTGGCAGAGCGGCCACGCCACCTTTATGTGTGTGATCCGATCTGGC	60
QY	283	ACCATGGGTGGAGCTTGTGGGTATGGGAATTTATACAGCCCAAGGGTATGGCAGCAACACGC	342
Db	61	ACCATGGGTGGAGCTTGTGGGTATGGGAATTTATACAGCCCAAGGGTATGGCAGCAACACGC	120
QY	343	GTGGCGCTGAGCACCTGCCTATTTAACAATGATTAAGTGTGTGCTTGCATTCGAAATG	402

Db 121 GTGGCGCTGAGCACTGGGCTATTAAACATGATTAAGTTGTGTGCTTGTGCAATG 180
 QY 403 ACTTGTAACAAAGCACTTAATGTGCTTCCGGAACTATTAGGGTCACTGCCACCAAC 462
 Db 181 ACTTGTAACAAAGCACTTAATGTGCTTCCGGAACTATTAGGGTCACTGCCACCAAC 240
 QY 463 TTTTGCCCTCTTAACCTTGTCTCTCCCTAAACAACATGTGATGTGCAACCTCTCTC 522
 Db 241 TTTTGCCCTCTTAACCTTGTCTCTCCCTAAACAACATGTGATGTGCAACCTCTCTC 300
 QY 523 CAACACTTGACATGGCTGAGCCCTGCTCTTCAAAATGCTCAATACGAGCTGTATC 582
 Db 301 CAACACTTGACATGGCTGAGCCCTGCTCTTCAAAATGCTCAATACGAGCTGTATC 360
 QY 583 GTCCCGCTCTCTTGTGAGGGTACATGTATGAAGAAAGGTGAGTGAAGTTTACATC 642
 Db 361 GTCCCGCTCTCTTGTGAGGGTACATGTATGAAGAAAGGTGAGTGAAGTTTACATC 420
 QY 643 AATGGCACTCATCTTCAACCTCGTTTGATCACAACGTCGGTGGCGCAGCGACGTC 702
 Db 421 AATGGCACTCATCTTCAACCTCGTTTGATCACAACGTCGGTGGCGCAGCGACGTC 480
 QY 703 CACTGTGTGATGAAGGGTCTCGAATGGAATGCAATGCTAGAAATTTGGGC 762
 Db 481 CACTGTGTGATGAAGGGTCTCGAATGGAATGCAATGCTAGAAATTTGGGC 540
 QY 763 CAAACTGGCAAGCAACACTATCTCAATGCGCAAGGCTTTCTTCAAGTCACTCTT 822
 Db 541 CAAACTGGCAAGCAACACTATCTCAATGCGCAAGGCTTTCTTCAAGTCACTCTT 600
 QY 823 AGTATGTGCGCACTCTCACTGCTATATCTGTTCTTCAATGCAATTTGGCCAA 882
 Db 601 AGTATGTGCGCACTCTCACTGCTATATCTGTTCTTCAATGCAATTTGGCCAA 660
 QY 883 ACCTATGAAGGCTCTCAATTC 903
 Db 661 ACCTATGAAGGCTCTCAATTC 681

RESULT 2

US-09-092-160-1
 ; Sequence 1, Application US/09092160C
 ; Patent No. 6255466
 ; GENERAL INFORMATION:
 ; APPLICANT: Cosgrove, Daniel J
 ; APPLICANT: McQueen-Mason, Simon
 ; APPLICANT: Guilthian, Mark J
 ; APPLICANT: Shcherban, Tatyana
 ; APPLICANT: Shi, Jun
 ; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
 ; FILE REFERENCE: 1194/1C114US3
 ; CURRENT APPLICATION NUMBER: US/09/092,160C
 ; EARLIER APPLICATION NUMBER: 08/440,517
 ; EARLIER FILING DATE: 1995-05-12
 ; EARLIER APPLICATION NUMBER: 08/242,090
 ; EARLIER FILING DATE: 1994-05-12
 ; EARLIER APPLICATION NUMBER: 08/060,944
 ; EARLIER FILING DATE: 1993-05-12
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 681
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: cDNA cucumber
 ; OTHER INFORMATION: expansin
 US-09-092-160-1

Query Match 68.6%; Score 681; DB 3; Length 681;
 Best Local Similarity 100.0%; Pred. No. 2e-197;
 Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 GACTACGGTGGCTGGCAGAGCGGCCACGCCACCTTTATGATGTGTGACGCAATCTGGC 282
 Db 1 GACTACGGTGGCTGGCAGAGCGGCCACGCCACCTTTATGATGTGTGACGCAATCTGGC 60
 QY 283 ACCATGGGTGAGCTTGTGGTATGGGAATTTATACAGCCAAAGGATATGACAGCAACG 342
 Db 61 ACCATGGGTGAGCTTGTGGTATGGGAATTTATACAGCCAAAGGATATGACAGCAACG 120
 QY 343 GTGGCGCTGAGCACTGGCGCTATTAAACATGATTAAGTTGTGCTTGTGCAATG 402
 Db 121 GTGGCGCTGAGCACTGGCGCTATTAAACATGATTAAGTTGTGCTTGTGCAATG 180
 QY 403 ACTTGTAACAAAGCACTTAATGTGCTTCCGGAACTATTAGGGTCACTGCCACCAAC 462
 Db 181 ACTTGTAACAAAGCACTTAATGTGCTTCCGGAACTATTAGGGTCACTGCCACCAAC 240
 QY 463 TTTTGCCCTCTTAACCTTGTCTCTCCCTAAACAACATGTGATGTGCAACCTCTCTC 522
 Db 241 TTTTGCCCTCTTAACCTTGTCTCTCCCTAAACAACATGTGATGTGCAACCTCTCTC 300
 QY 523 CAACACTTGACATGGCTGAGCCCTGCTCTTCAAAATGCTCAATACGAGCTGTATC 582
 Db 301 CAACACTTGACATGGCTGAGCCCTGCTCTTCAAAATGCTCAATACGAGCTGTATC 360
 QY 583 GTCCCGCTCTCTTGTGAGGGTACATGTATGAAGAAAGGTGAGTGAAGTTTACATC 642
 Db 361 GTCCCGCTCTCTTGTGAGGGTACATGTATGAAGAAAGGTGAGTGAAGTTTACATC 420
 QY 643 AATGGCACTCATCTTCAACCTCGTTTGATCACAACGTCGGTGGCGCAGCGACGTC 702
 Db 421 AATGGCACTCATCTTCAACCTCGTTTGATCACAACGTCGGTGGCGCAGCGACGTC 480
 QY 703 CACTGTGTGATGAAGGGTCTCGAATGGAATGCAATGCTAGAAATTTGGGC 762
 Db 481 CACTGTGTGATGAAGGGTCTCGAATGGAATGCAATGCTAGAAATTTGGGC 540
 QY 763 CAAACTGGCAAGCAACACTATCTCAATGCGCAAGGCTTTCTTCAAGTCACTCTT 822
 Db 541 CAAACTGGCAAGCAACACTATCTCAATGCGCAAGGCTTTCTTCAAGTCACTCTT 600
 QY 823 AGTATGTGCGCACTCTCACTGCTATATCTGTTCTTCAATGCAATTTGGCCAA 882
 Db 601 AGTATGTGCGCACTCTCACTGCTATATCTGTTCTTCAATGCAATTTGGCCAA 660
 QY 883 ACCTATGAAGGCTCTCAATTC 903
 Db 661 ACCTATGAAGGCTCTCAATTC 681

RESULT 3

US-08-845-539-5
 ; Sequence 5, Application US/08845539
 ; Patent No. 5929303
 ; GENERAL INFORMATION:
 ; APPLICANT: Bennett, Alan B.
 ; APPLICANT: Rose, Jocelyn K.C.
 ; TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
 ; TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:


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1 MEDIUM TYPE: Floppy disk
2 COMPUTER: IBM PC compatible
3 OPERATING SYSTEM: PC-DOS/MS-DOS
4 SOFTWARE: Microsoft word
5 CURRENT APPLICATION DATA:
6 APPLICATION NUMBER: US/07/885,970A
7 FILING DATE: 19920518
8 CLASSIFICATION: 435
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: US 07/617,239
11 FILING DATE: 21-NOV-1990
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: US 07/253,243
14 FILING DATE: 04-OCT-1988
15 ATTORNEY/AGENT INFORMATION:
16 NAME: Seay, Nicholas J.
17 REGISTRATION NUMBER: 27,386
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: (608) 283-2478
20 TELEFAX: (608) 251-5139
21 INFORMATION FOR SEQ ID NO: 6:
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 727 base pairs
24 TYPE: NUCLEIC ACID
25 STRANDEDNESS: double
26 TOPOLOGY: linear
27 MOLECULE TYPE: CDNA
28 HYPOTHETICAL: NO
29 ANTI-SENSE: NO
30 ORIGINAL SOURCE:
31 ORGANISM: Gossypium hirsutum
32 STRAIN: Coker 312
33 DEVELOPMENTAL STAGE: 10 day old fiber cells
34 TISSUE TYPE: fiber cells
35 IMMEDIATE SOURCE:
36 LIBRARY: CKB10
37 CLONE: B12
38
39 US-07-885-970A-6

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Query Match	26.5%;	Score 262.6;	DB 1;	Length 727;
Best Local Similarity	72.5%;	Pred. No. 4.5e-70;		
Matches 340; Conservative	0;	Mismatches 129;	Indels 0;	Gaps 0;

QY	442	ATTAGGGTCACTGCCACCAACTTTGGCCCTCTAACTTTGCTCCCTTAACAACAATGCT	501
Db	1	ATAACCGTGACAGCCCAACTTTGTCTCACTTAAGTCTTTATCTAGTACAATGGC	60
QY	502	GGATGCGTCAACCCCTCTCTCCAACACTTCGACATGGCTGAGCCCTGCTTCTCAATC	561
Db	61	GGGTGCTCAATCCCCCAGAGAACACTTTGATTGGCCGAAACGGCATTCTTGCCGATA	120
QY	562	GCTCAATACCAGGCTGTATCGTCCCGTCTCCTTTGTAAGGTATCCATGTATGAAGAA	621
Db	121	GCAGAAATATCGAGCTGGAATCGTCCCTGTATTATGTTCAAGAAAGGTGTCAATGTGTGAAGAA	180
QY	622	GGTGAAGTGAGGTTTACAATCAATGGCCACTCATCTTCAACCTCGTTTGAATCACAAAC	681
Db	181	GGAGGCATCAGGTACACCATGAATGACATTCTGACTTCAACATGGTGTGATTAACGAAC	240
QY	682	GTGCGTGGCGCAGGCGCAGTCCACTCTGTGTGATAAAGGGGCTCGAACTGGATGGCAA	741
Db	241	GTGGAGGGGGCAGGGGATATAACGTCACTGTCCATCAAGGGTTCCAGAAACGAGATGGCTA	300
QY	742	TCCATGTCTAGAAATTGGGGCCAAAACCTGGCAAAAGCAACAATATCTCAAATGGCCAAAGC	801
Db	301	CCATATGTCAGAAATTGGGGCCAAAACCTGGCAGAGCAATGCTTACCTTAAACGACAAAGC	360
QY	802	CTTTCCTTTCAAGTCACTCTTAGTGATGCTGCACCTCTCACTGCCTATAAATCTCGTTCT	861
Db	361	CTCTCTTTAAAGTGAAGTGCACAGCGATGGCAGAGACTATCAACAGCTACAAATGTAGTGCT	420
QY	862	TCCAATTGGCAATTTGGCCAAACCTATGAAGGCCCTCAATTCTTAACCA	910

Db 421 GCTGGTTGCCAATTTCGACAAACTTTTGAAGGAGGCCAGTTTAAACA 469

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US-08-298-687A-6
; Sequence 6, Application US/08298687A
; Patent No. 5521078
;
; GENERAL INFORMATION:
; APPLICANT: John, Mallyakal E.
; TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
; TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nicholas J. Seay, Quarles & Brady
; STREET: P.O. Box 2113, First Wisconsin Plaza
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53701
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/298,687A
; FILING DATE:
;
; CLASSIFICATION: 800
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/617,239
; FILING DATE: 21-NOV-1990
;
; PRIOR APPLICATION NUMBER: US 07/253,243
; APPLICATION NUMBER: 04-OCT-1988
; FILING DATE: 04-OCT-1988
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 283-2478
; TELEFAX: (608) 251-5139
;
; INFORMATION FOR SEQ ID NO: 6:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 727 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
; ORIGINAL SOURCE:
; ORGANISM: Gossypium hirsutum
; STRAIN: Coker 312
; DEVELOPMENTAL STAGE: 10 day old fiber cells
; TISSUE TYPE: fiber cells
; IMMEDIATE SOURCE:
;
; LIBRARY: CKB10
; CLONE: B12
;
US-08-298-687A-6

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Query Match	26.5%;	Score 262.6;	DB 1;	Length 727;
Best Local Similarity	72.5%;	Pred. No. 4.5e-70;		
Matches 340; Conservative	0;	Mismatches 129;	Indels 0;	Gaps 0;

[illegible]


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Db 121 GCAGATATCGAGCTGGAATCGTCCCTGTTATGTTCAAGAGGGTGTGTAAGAAA 180
QY 622 GGTGAGTAGAGTTTACATCAATGAGCCACTCATCTTCAACCTGTTTATGATCAAAAC 681
Db 181 GGAGGCATCAGGTACACCATGAAATGACATTCGTACTTCAACATGTTGTTATGATGCAAC 240
QY 682 GTGGGTGGCGCAGGCGACGCTCATCTGTGTGATTAAGGGGTCTGCACTGATGGCAA 741
Db 241 GTGGGAGGGGCGAGGGGATATTAACGTCAGTGTCCATCAAGGGTTCAGAACAGATGGCTA 300
QY 742 TCCATGTCTAGAAATGGGGCCAAACTGGCAAGCAACAATCTCAATGGCCAAAGC 801
Db 301 CCTATGTCCAGAAATGGGGCCAAACTGGCAGAGCAATGCTTACCTTAACGGAACAAGC 360
QY 802 CTTTCCTTTCAAGTCACTCTTAGTGTGTGCGACTCTCACTGCTATATCTGTTCCCT 861
Db 361 CTCTCTTTTAAAGTACTGCGCAGGATGGCAGACTATCACAGCCTACATGTAGTGCCT 420
QY 862 TCCAAATTGGCAATTGGCCAAACCTATGAAGGCCCTCAATTCTAAACCA 910
Db 421 GCTGTTGGCAATTGGCAAACTTTTGAAGAGGCCAGTTTAAAGACA 469

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RESULT 7
US-08-530-797-5

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; Sequence 5, Application US/08530797
; Patent No. 5597718
; GENERAL INFORMATION:
; APPLICANT: John, Maliyakal E.
; APPLICANT: Umbeck, Paul F.
; APPLICANT: Brill, Winston J.
; TITLE OF INVENTION: GENETICALLY ENGINEERED COTTON PLANTS
; TITLE OF INVENTION: FOR ALTERED FIBER
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles and Brady
; STREET: P.O. Box 2113
; STREET: FIRST WISCONSIN PLAZA
; CITY: MADISON
; STATE: WISCONSIN
; COUNTRY: U.S.A.
; ZIP: 53701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 800Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,797
; FILING DATE: 20-SEP-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/617,239
; FILING DATE: 21-NOV-90
; APPLICATION NUMBER: US 07/253,243
; FILING DATE: 04-OCT-88
; ATTORNEY/AGENT INFORMATION:
; NAME: Nicholas J. Seay
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 1122990245
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 727 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Gossypium hirsutum
; STRAIN: Coker 312
; DEVELOPMENTAL STAGE: 10 day old fiber cells

```

```

; TISSUE TYPE: fiber cells
; IMMEDIATE SOURCE:
; LIBRARY: CKFB10
; CLONE: B12
; US-08-530-797-5

```

Query Match 26.5%; Score 262.6; DB 1; Length 727;
Best Local Similarity 72.5%; Pred. No. 4.5e-70;
Matches 340; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

```

QY 442 ATTAGGTCACCTCCACCACTTTTGGCCCTCACTTGTCTCCCTAACACAATGTGT 501
Db 1 ATAAACGTCAGACCCACCACTTTTGTCCACTACTATGCTTTATCTAGTGAATGGC 60
QY 502 GGATGTCACACCCCTCTCCACACACTTGCACATGCGTGAAGCCCTGCTTCAATC 561
Db 61 GGGTGTGCAATCCCCCAGAGAACACTTTGATTTGGCCGACCGGCAATCTTCCGGATA 120
QY 562 GCTCAATACCGAGCTGTATGCTCCCGCTCTCTTCTTGTAGGGTACCATGTATGAAGAA 621
Db 121 GCAGATATCGAGCTGGAATGCTCCCTGTTATGTTCAAGAGGGTGTATGTGTAAGAAA 180
QY 622 GGTGAGTAGAGTTTACATCAATGAGCCACTCATCTTCAACCTGTTTATGATCAAAAC 681
Db 181 GGAGGCATCAGGTACACCATGAAATGACATTCGTACTTCAACATGTTGTTATGATGCAAC 240
QY 682 GTGGGTGGCGCAGGCGACGCTCATCTGTGTGATTAAGGGGTCTGCACTGATGGCAA 741
Db 241 GTGGGAGGGGCGAGGGATATTAACGTCAGTGTTCATCAAGGGTTCAGAACAGATGGCTA 300
QY 742 TCCATGTCTAGAAATGGGGCCAAACTGGCAAGCAACAATCTCAATGGCCAAAGC 801
Db 301 CCTATGTCCAGAAATGGGGCCAAACTGGCAGAGCAATGCTTACCTTAACGGAACAAGC 360
QY 802 CTTTCCTTTCAAGTCACTCTTAGTGTGTGCGACTCTCACTGCTATATCTGTTCCCT 861
Db 361 CTCTCTTTTAAAGTACTGCGCAGGATGGCAGACTATCACAGCCTACATGTAGTGCCT 420
QY 862 TCCAAATTGGCAATTGGCCAAACCTATGAAGGCCCTCAATTCTAAACCA 910
Db 421 GCTGTTGGCAATTGGCAAACTTTTGAAGAGGCCAGTTTAAAGACA 469

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RESULT 8

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; US-08-298-829-6
; Sequence 6, Application US/08298829
; Patent No. 5620882
; GENERAL INFORMATION:
; APPLICANT: John, Maliyakal E.
; TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
; TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nicholas J. Seay, Quarles & Brady
; STREET: P.O. Box 2113, First Wisconsin Plaza
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/298,829
; FILING DATE: 19-OCT-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/885,970
; FILING DATE: 18-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/617,239

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; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/253,243
; FILING DATE: 04-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 283-2478
; TELEFAX: (608) 251-5139
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 727 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Gossypium hirsutum
; STRAIN: Coker 312
; DEVELOPMENTAL STAGE: 10 day old fiber cells
; TISSUE TYPE: fiber cells
; IMMEDIATE SOURCE:
; LIBRARY: CKFB10
; CLONE: B12
; US-08-298-829-6

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Query Match      26.5%; Score 262.6; DB 1; Length 727;
Best Local Similarity 72.5%; Pred. No. 4.5e-70;
Matches 340; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

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QY 442 ATTAGGTCACCTGACCACTTTGGCCCTCTTAACCTTGTCTCCCTAACCAACATGCT 501
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Db 1 ATAACTGACAGCCACCACTTTGTCACCTAATGCTTATCTAGTGAACATGCG 60
QY 502 GGATGTCACACCTCTCTCTCCACACTTGCATGCTGAGCCCTGCTCTTCAATC 561
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Db 61 GGGTGTGCAATCCCAACGAGAACACTTTGATTTGGCGAACCGCAATCTTGCGATA 120
QY 562 GCTCAATACCGAGCTGTATGTCCTCCCTCTCTTTCGTAAGGTACATGATGAAGAA 621
   |||||
Db 121 GCAGATATGAGCTGGAATGCTCCCTGTATGTCAGAAAGGTGTCATGTGTAAGAA 180
QY 622 GGTGAGTGAGGTTTACATCAATGAGCACTCATACTTCAACCTCGTTTGATCAACA 681
   |||||
Db 181 GGAGCATCAGGTACACCATGATGACATTCGTAATTCAACATGCTTGAATGAAGAAC 240
QY 682 GTGCGTGGCGAGCGACGTCACCTGTGTGATGAAGGGGTCTCGAATGATGCGAA 741
   |||||
Db 241 GTGGAGGGGCGAGGGGATATAACGTGCTGTCATCAAGGGTTCAGAACAGATGCTA 300
QY 742 TCCATGCTAGAAATTTGGGCAAAATGCGCAAAAGCAACAATATCTCAATGCGCAAGC 801
   |||||
Db 301 CCTATGTCAGAAATTTGGGCAAAATGCGCAAGCAATGCTTACCTTAACGAGCAAGC 360
QY 802 CTTTCCTTCAAGTCACTTGTAGTGTGCTGCACTCTCACTGCTTCAATCTGCTTCT 861
   |||||
Db 361 CTCTCTTTAAAGTACTGCGAGCAATGAGCAAGACTATCAACGCTTCAATGATGCT 420
QY 862 TCCATGCGCAATTTGGCAAACTATGAAGGCTCTCAATCTTAACCA 910
   |||||
Db 421 GCTGTTGGCAATTCGCAAACTTTGAAGAGGCGCAATTTTAAGACA 469

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RESULT 9
US-08-787-335-5
; Sequence 5, Application US/08787335
; Patent No. 5981834
; GENERAL INFORMATION:
; APPLICANT: John, Maliyakal E.
; APPLICANT: Umbeck, Paul F.

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; APPLICANT: Brill, Winston J.
; TITLE OF INVENTION: GENETICALLY ENGINEERED COTTON PLANTS
; TITLE OF INVENTION: FOR ALTERED FIBER
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles and Brady
; STREET: P.O. BOX 2113
; CITY: MADISON
; STATE: WISCONSIN
; COUNTRY: U.S.A.
; ZIP: 53701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 800Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,335
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/530,797
; FILING DATE:
; APPLICATION NUMBER: US 07/253,243
; FILING DATE: 04-OCT-88
; ATTORNEY/AGENT INFORMATION:
; NAME: Nicholas J. Seay
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 1122990245
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 727 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Gossypium hirsutum
; STRAIN: Coker 312
; DEVELOPMENTAL STAGE: 10 day old fiber cells
; TISSUE TYPE: fiber cells
; IMMEDIATE SOURCE:
; LIBRARY: CKFB10
; CLONE: B12
; US-08-787-335-5

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Query Match      26.5%; Score 262.6; DB 2; Length 727;
Best Local Similarity 72.5%; Pred. No. 4.5e-70;
Matches 340; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

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QY 442 ATTAGGTCACCTGACCACTTTGGCCCTCTTAACCTTGTCTCCCTAACCAACATGCT 501
   |||||
Db 1 ATAACTGACAGCCACCACTTTGTCACCTAATGCTTATCTAGTGAACATGCG 60
QY 502 GGATGTCACACCTCTCTCTCCACACTTGCATGCTGAGCCCTGCTCTTCAATC 561
   |||||
Db 61 GGGTGTGCAATCCCAACGAGAACACTTTGATTTGGCGAACCGCAATCTTGCGATA 120
QY 562 GCTCAATACCGAGCTGTATGTCCTCCCTCTCTTTCGTAAGGTACATGATGAAGAA 621
   |||||
Db 121 GCAGATATGAGCTGGAATGCTCCCTGTATGTCAGAAAGGTGTCATGTGTAAGAA 180
QY 622 GGTGAGTGAGGTTTACATCAATGAGCACTCATACTTCAACCTCGTTTGATCAACA 681
   |||||
Db 181 GGAGCATCAGGTACACCATGATGACATTCGTAATTCAACATGCTTGAATGAAGAAC 240
QY 682 GTGCGTGGCGAGCGACGTCACCTGTGTGATGAAGGGGTCTCGAATGATGCGCAA 741
   |||||
Db 241 GTGGAGGGGCGAGGGGATATAACGTGCTGTCATCAAGGGTTCAGAACAGATGCGCTA 300

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QY 742 TCATGCTAGAAATGGGGCCAAACTGCGCAACAACTATCTCAATGGCCAGGC 801
 DB 301 CTTATGTCAGAAATGGGGCCAAACTGCGAGCAATGCTTAAACGCAAGC 360
 QY 802 CTTTCCTTCAAGTCACTCTTAGTGTGCGCACTCTCACTGCTTAACTGTTCT 861
 DB 361 CTCTCTTTAAAGTACTGCCAGCGATGGCAGACTATCACAGCTTAACTGTTAGT 420
 QY 862 TCCATTGGCAATTTGGCCAACTATGAAGCCCTCAATTCTAAACCA 910
 DB 421 GCTGTTGGCAATTCGACAACTTTGAAGAGGCCAGCTTTAAAGACA 469

RESULT 10

US-07-885-970A-26
 ; Sequence 26, Application US/07885970A
 ; Patent No. 5495070
 ; GENERAL INFORMATION:
 ; APPLICANT: John, Maliyakal E.
 ; TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nicholas J. Seay, Quarles & Brady
 ; STREET: P.O. Box 2113, First Wisconsin Plaza
 ; CITY: Madison
 ; STATE: Wisconsin
 ; COUNTRY: USA
 ; ZIP: 53701
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Microsoft Word
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 19920518
 ; APPLICATION NUMBER: US/07/885,970A
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/617,239
 ; FILING DATE: 21-NOV-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/253,243
 ; FILING DATE: 04-OCT-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seay, Nicholas J.
 ; REGISTRATION NUMBER: 27,386
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (608) 283-2478
 ; TELEFAX: (608) 251-5139
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2415 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Gossypium barbadense
 ; STRAIN: Sea Island
 ; IMMEDIATE SOURCE:
 ; LIBRARY: EMBL SI
 ; CLONE: SIB12
 ; US-07-885-970A-26

Query Match 25.9%; Score 256.6; DB 1; Length 2415;
 Best Local Similarity 64.6%; Pred. No. 5.9e-68;
 Matches 458; Conservative 0; Mismatches 174; Indels 77; Gaps 2;

QY 279 TGGACCATGGGTGAGCTTGTGGGTATGGGAATTATACAGCCAGGATGACGAGAA 338
 DB 976 TGTTCCTATAGGGGAGCTTGTGTTATGAAACCTGTACAGTCAAGGATGGAACGAG 1035

QY 339 CACGGTGGCCTGAGCACTGGGCTATTTAACAATGATTAAGTGTGTGC-TTGCTTGC 397
 DB 1036 CACAGCAGCTTTGAGCACTGCACTTTTCAACAATGGCTTGAGCTGCGGTGCACTGACG 1095
 QY 398 AATGACTTGTACAACGACCTAAATGCTGCTTCCGGAACTATTAGGCTCACTGCA 457
 DB 1096 AGCTCCGGTCAACAATGATCTCAATGCTGATTAAGTCAATTAACCGTGAACGCA 1155
 QY 458 CCAACTTTGCTCCCTTCACTTTGCTCTCCCTTAACAACAATGCTGATGTCACACCTC 517
 DB 1156 CCAACTTTGCTCCCTTCACTTTATCTTATGATGACAAATGGCGGTGTCATCCCC 1215
 QY 518 CTCTCAACACTTGCACATGCTGAGCCTGCTCTTCTTCAAAATGCTCAATACCGAGCTG 577
 DB 1216 CACGAGAACACTTTGATTTGGCCGAACCGCATTTCTGAGATCGCGAATATCGAGCTG 1275
 QY 578 GTATCGTCCCG-----TCTCCTTTGTTAGGTTACCATGATGAAGAA 589
 DB 1276 GAATCGTCCCTGTTATGTCAGAGGTGTAATAAATCAATTCAATCATCACTC 1335
 QY 590 -----TCTCCTTTGTTAGGTTACCATGATGAAGAA 621
 DB 1336 TTTAAGTATGTTAACTGTTGGGTGTTAACTTTTGCAAGGTGTCATGTTGAAGAA 1395
 QY 622 GGTGAGTGAAGTTTAACTCAATGAGCACTCATACTTCAACTGTTTATGATCACAAC 681
 DB 1396 GAGGATCAGTACATGACATGATGACATGCTACTTCAACATGTTGATTAACCAAC 1455
 QY 682 GTGCGTGGCGCAGCGAGCTCCACTCTGTGTCGATAAAGGGTCTCGAATGATGAGCA 741
 DB 1456 GTGAGAGGGGCAAGGATTAACGTCACTGTCATCAAGTGTCCAAACAGATGAGCTA 1515
 QY 742 TCCATGCTAGAATTTGGGGCCAAACTGCGCAACAACTATCTCAATGGCCAGGC 801
 DB 1516 CTTATGTCAGAAATTTGGGGCCAAACTGCGCAACAACTATCTCAATGGCCAGGC 1575
 QY 802 CTTTCCTTCAAGTCACTCTTAGTGTGCGCACTCTCACTGCTTAACTGTTCTCT 861
 DB 1576 CTCTCTTTCAAGTCACTGCGCAGATGCGAGACTATCAAACTAATGATGCTCT 1635
 QY 862 TCCATTGGCAATTTGGCCAACTATGAAGCCCTCAATTCTAAACCA 910
 DB 1636 GCTGTTGGCAATTCGACAACTTTGAAGAGGCCAGCTTTTAAGACA 1684

RESULT 11

US-08-298-687A-26
 ; Sequence 26, Application US/08298687A
 ; Patent No. 5521078
 ; GENERAL INFORMATION:
 ; APPLICANT: John, Maliyakal E.
 ; TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nicholas J. Seay, Quarles & Brady
 ; STREET: P.O. Box 2113, First Wisconsin Plaza
 ; CITY: Madison
 ; STATE: Wisconsin
 ; COUNTRY: USA
 ; ZIP: 53701
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Microsoft Word
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 08/298,687A
 ; APPLICATION NUMBER: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/617,239

FILING DATE: 21-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/253,243
 FILING DATE: 04-OCT-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27,386
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (608) 283-2478
 TELEFAX: (608) 251-5139
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2415 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Gossypium barbadense
 STRAIN: Sea Island
 IMMEDIATE SOURCE:
 LIBRARY: EMBL-SI
 CLONE: SIB12
 US-08-298-687A-26

Query Match 25.9%; Score 256.6; DB 1; Length 2415;
 Best Local Similarity 64.6%; Pred. No. 5.9e-68;
 Matches 458; Conservative 0; Mismatches 174; Indels 77; Gaps 2;

QY 279 TGGCACCATTGGGAGCTTGGGATTTATATACAGCCAGGATGACAGAA 338
 DB 976 TGTTCATATAGGGGAGCTTGTGTTATGAAACCTGTACAGTCAAGGTTATGAAACAG 1035
 QY 339 CACGGTGGCGCTGAGCACTGCGCTATTTAACAATGATTAAGTTGCTGC-TTGCTTCG 397
 DB 1036 CACAGACGCTTGAGCACTGCACTTTTCAACAATGCTGAGCTGCGGTGCACTGCTACG 1095
 QY 398 AATGACTGTATCAAAACGACCTTAATGCTGCTCCGGGAATTAAGGTCACCTGCA 457
 DB 1096 AGCTCCGGTGCAACATGATCTCAATGCTGATGCAACCATTAACCGTGACAGCA 1155
 QY 458 CCAACTTTTGGCCCTCTAATCTTGTCTCTCCCTAACAACAATGCTGATGTCACCTC 517
 DB 1156 CCAACTTTTGTCCCTTAATCTATGCTTATCTAGTACAAATGCGGGTGTCAATCCC 1215
 QY 518 CTCTCCAACTTGCACATGCTGAGCTGCTCTCTCTCAATGCTCAATACCGAGCTG 577
 DB 1216 CACGAGACACTTGTATTTGGCCGAAACCGCATTTCTGAGATCGCGAATATGAGCTG 1275
 QY 578 GTATGTCCTCCG-----TCTCTTCTGAGGATACCATGTATGAAGAA 589
 DB 1276 GAATGTCCTCTTATGTTCAAGAGTGATGAATAAACTCAATTCAATCATCACACTC 1335
 QY 590 -----TCTCTTCTGAGGATACCATGTATGAAGAA 621
 DB 1336 TTTAAGTATGTTAACTGTGGGTGTTAACTTTTGAAGGCTGTATGTGAAGAA 1395
 QY 622 GGTGAGTGAAGTTTACATCAATGCTGCTCATCTCACTCACTGTTTGTATGACAAAC 681
 DB 1396 GGAGGATCAGGTACACCATGATGACATGCTGCTCAATGCTGATGATTAACCAAC 1455
 QY 682 GTGGTGGCGAGGAGCTCCACTCTGTGTGATTAAGGGGTCTGAACTGATGAGCA 741
 DB 1456 GTGGAGGGGCAAGGATATTAACGTGCTGCTCATCAAGTGTTCAAAACAGGATGCTA 1515
 QY 742 TCCATGTTAGAAATTTGGGCAAAACCTGGCAAGCAACTATCTCAATGGCCAAAGC 801
 DB 1516 CTTATGTCAGAAATTTGGGCAAAACCTGGCAAGCAACTATCTCAATGGCCAAAGC 1575
 QY 802 CTTTCTTCAAGTCACTCTTAAGTGTGCTGCACTGCTCACTGCTATATCTGCTTCT 861

DB 1576 CTCTCTTCAAGTGAAGTCCAGCGATGGCAGAGCTATCACAACCTAATGATGCTCCT 1635
 QY 862 TCCATTTGGCAATTTGGCCAACTATGAAGGCTCAATCTTAACCA 910
 DB 1636 GCTGCTTGGCAATTCGACAACTTTTGAAGGAGGCCAGTTTAAAGACA 1684

RESULT 12
 US-08-298-829-26
 Sequence 26, Application US/08298829
 Patent No. 5620882

GENERAL INFORMATION:
 APPLICANT: John, Maliyakal E.
 TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
 TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nicholas J. Seay, Quarles & Brady
 STREET: P.O. Box 2113, First Wisconsin Plaza
 CITY: Madison
 STATE: Wisconsin
 COUNTRY: USA

ZIP: 53701
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/298,829
 FILING DATE: 19-OCT-1994
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/885,970
 FILING DATE: 18-MAY-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/617,239
 FILING DATE: 21-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/253,243
 FILING DATE: 04-OCT-1988

ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27,386
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (608) 283-2478
 TELEFAX: (608) 251-5139

INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2415 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO

ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Gossypium barbadense
 STRAIN: Sea Island
 IMMEDIATE SOURCE:
 LIBRARY: EMBL-SI
 CLONE: SIB12
 US-08-298-829-26

Query Match 25.9%; Score 256.6; DB 1; Length 2415;
 Best Local Similarity 64.6%; Pred. No. 5.9e-68;
 Matches 458; Conservative 0; Mismatches 174; Indels 77; Gaps 2;

QY 279 TGGCACCATTGGGAGCTTGGGATTTATATACAGCCAGGATGACAGAA 338
 DB 976 TGTTCATATAGGGGAGCTTGTGTTATGAAACCTGTACAGTCAAGGTTATGAAACAG 1035
 QY 339 CACGGTGGCGCTGAGCACTGCGCTATTTAACAATGATTAAGTTGCTGC-TTGCTTCG 397

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Db 1036 CACAGACGCTTGAGCACTGCACTTTTCAACAATGGCTTGAGCTGCGGTGCACTGCTACG 1095
QY 398 AAATGACTTTGACAAACGACCCCTTAATGTGCTCTCCGGAACTATTAGGGTCACTGCCA 457
Db 1096 AGCTCCGGTGCAACATGATCTCTCAATGTTAGTGAACATAACCGTGACAGCCA 1155
QY 458 CCAACTTTGGCCCTCTTAACCTTCTCTCCCTTAACAACAATGGTGGATGGTGAACCCCTC 517
Db 1156 CCAACTTTGTCCTCCCTTAACCTTCTCTCTCTTAAGTGAACAATGGCGGGTGGTGAATCCC 1215
QY 518 CTCTCCAACACTTGCACATGGCTGAGCCCTGCTCTCTCAATCGCTCAATACGAGCTG 577
Db 1216 CACGAGAACACTTGTATTGGCCGAACCGGCACTTCTGAGATCGCGAATATCGAGCTG 1275
QY 578 GTATCGTCCCG----- 589
Db 1276 GAATCGTCCCTGTTATGTTGAGAGGTGTGAATAAACTCAATTCAAATCATCACACTC 1335
QY 590 -----TCTCCTTTCGTAGGGTACCATGTATGAAGAA 621
Db 1336 TTTAAGGTATGTTAACTGTGGGTGTTTAACTTTTGAGGGTGTCAATGTGAAGAA 1395
QY 622 GGTGAGTGAAGTTTACATCATGAGCCACTCATCTTCAACCTCGTTTGTATCAACAAC 681
Db 1396 GGAGGATCAGGTACACCATGATGACATGTACTTCAACATGTGTGTTGATTAACCAAC 1455
QY 682 GTGGGTGGCGAGCGCAGCTCACTGTGTGATTAAGGGGTCTGCAACTGATGCAAA 741
Db 1456 GTGGAGGGGAGGGGATATATAGTCACTGTCATCAAGTGTCCAAAACAGATGGCTA 1515
QY 742 TCCATGCTAGAAATGGGGCCAAACTGGCAAGCAACAATCTCAATGGCCCAAGC 801
Db 1516 CCTATGTCAGAAATGGGGCCAAACTGGCAAGCAATGCTTAACGAGCCCAAGC 1575
QY 802 CTTCTCTTCAAGTCACTCTTATGATGTGTGCACTCTCACTGCTTATATCTGCTCT 861
Db 1576 CTCTCTTCAAGTCACTGTCAGCGAGTGGAGACTATCAACAATCAATGATGCTCT 1635
QY 862 TCCAAATGGCAATTTGGCCAACTATGAAGGCCCTCAATTTCAACCA 910
Db 1636 GCTGTTGGCAATTCGACAACTTTGAAGAGGCGCAGTTTAAGACA 1684
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RESULT 13

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US-08-845-539-1
; Sequence 1, Application US/08845539
; Patent No. 5929303
; GENERAL INFORMATION:
; APPLICANT: Bennett, Alan B.
; APPLICANT: Rose, Jocelyn K.C.
; TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
; TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,539
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
```

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; REFERENCE/DOCKET NUMBER: 023070-078200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 28..702
; OTHER INFORMATION: /product="tomato lcbx1"
; US-08-845-539-1
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Query Match 25.4%; Score 251.6; DB 2; Length 702;
Best Local Similarity 67.2%; Pred. No. 9.8e-67;
Matches 391; Conservative 0; Mismatches 179; Indels 12; Gaps 2;
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QY 229 GGTGCTGCGAGAGCGGCCACCCCTTTATGTTGTTGTTGAGCATCTGCGACCATG 288
Db 118 GGTTCATGGAAACTGACATGCTACATTTTACGCGAAGTATGCTTGGAAACATG 177
QY 289 GGTGAGCTTGTGGTATGGGAATTTATACAGCCAAAGGTATGACAGAACAGGTGCG 348
Db 178 GCGGTGCGTGTGTTATGAATTTATACAGCCAAAGATACGAGTTAACAGACAGCA 237
QY 349 CTGAGCATGCGCTATTTAAATGATTAAGTTGTGTGCTTCTTCAATATGACTTGT 408
Db 238 CTGAGTACTCTTGTATTAACATGATTAAGTTGTGAGCTGTTTGAATTAATGT 297
QY 409 ACAACGACCT-----AAATGTCCTTCCGGAA-----CTATTAGGCTCACTGCC 456
Db 298 ACAATATCTCTAATTTGAATGTGTCTTCTGGAACCTTCCATTTAATCACAGCT 357
QY 457 ACCAATTTTCCCTCTCTAATCTTGTCTTCCCTAACACAACAATGTTGATGTCACACCT 516
Db 358 ACCAATTTTCCCTCTCTAATCTTGTCTTCCCTAACACAACAATGTTGATGTCACACCT 417
QY 517 CCTCTCCACACTTGCACATGCGCTGAGCTGCTCTCTCAATGCTCAATACCGAGCT 576
Db 418 CTTGCTCTCACTTGTGACCTGCTATGCTTCTCAACTTGTCTCACTGCTCACTGCT 477
QY 577 GGTATGTCCTCCCTCTCTCTTCTGTAAGGATCATGTATGAAGAAAGTGAAGTGT 636
Db 478 GGCATGTTCTCTGTAATCTATGCAAGATCCATGCCGAAGCAAGAGATCAAGATTT 537
QY 637 ACAATCAATGGCCACTCATCTTCACTCTGTTTGTATCAACAACGTCGTCGCGCAGC 696
Db 538 ACCATCAATGATTCGCTTACTTCACTTATGTTGATCAAGATGATGAGGTCAGGG 597
QY 697 GACGTCCACTCTGTGTGATTAAGGGGTCTGCACTGATGCAATCCATGCTAGAAT 756
Db 598 GATATTATTAAAGTTTGGGTAAAGGAACAAGACAATGATTCATTTGAGCCGTAA 657
QY 757 TGGGGCCAAACTGGCAAGCAACAACATCTCAATGCGCAA 798
Db 658 TGGGGCAAAATTTGCAATCAATATGCGGTTTAACTGTCAA 699
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RESULT 14

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US-09-362-642-1
; Sequence 1, Application US/09362642
; Patent No. 6350935
; GENERAL INFORMATION:
; APPLICANT: Bennett, Alan B.
; APPLICANT: Rose, Jocelyn K.C.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
; TITLE OF INVENTION: to Control Fruit Texture and Softening
; FILE REFERENCE: 023070-078210US
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Search completed: December 18, 2003, 22:33:40
Job time : 91 secs

1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2003, 19:50:59 ; Search time 314 Seconds
(without alignments)
8528.161 Million cell updates/sec

Title: US-09-383-579C-9

Perfect score: 992
Sequence: 1 gaataatcaacaacattgc.....aacacaaaacgcgaacgac 992

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_19Jun03:*

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- 21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
- 25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	684	69.0	684	ABA97161	C. sativus DNA enc
2	681	68.6	681	AAT13320	Cucumber expansin-
3	676.2	68.2	681	ABA97162	C. sativus DNA enc
4	404.4	40.8	1144	AAD32964	Pear expansin 2 (E
5	398.8	40.2	1015	AAC48712	Arabidopsis thalia
6	398.8	40.2	1016	AAC40777	Arabidopsis thalia
7	394.2	39.7	762	ABZ13283	Arabidopsis thalia
8	377.8	38.1	780	AAC50628	Arabidopsis thalia

9	377.8	38.1	1198	21	AAC33521	Arabidopsis thalia
10	377.8	38.1	1233	21	AAC50633	Arabidopsis thalia
11	366.8	37.0	1236	21	AAC40035	Arabidopsis thalia
12	361.8	36.5	687	24	ABA97164	N. tabacum DNA enc
13	360.6	36.4	753	24	ABZ12286	Arabidopsis thalia
14	360.4	36.3	747	24	ABZ13264	Arabidopsis thalia
15	360.4	36.3	1324	21	AAC47530	Arabidopsis thalia
16	354	35.7	1326	21	AAC40169	Arabidopsis thalia
17	351.4	35.4	1212	21	AAC45165	Arabidopsis thalia
18	341.6	34.4	1366	21	AAC47991	Arabidopsis thalia
19	341.6	34.4	774	24	ABZ12284	Arabidopsis thalia
20	341.6	34.4	1319	21	AAC44930	Arabidopsis thalia
21	338.4	34.1	1205	21	AAC33121	Arabidopsis thalia
22	338.2	34.1	1167	22	AAD03713	Tomato seed expans
23	332	33.5	1201	21	AAC44975	Arabidopsis thalia
24	321.8	32.4	1276	24	AAD32963	Pear expansin 1 (E
25	316.6	31.9	1236	21	AAC34714	Arabidopsis thalia
26	313.6	31.6	488	21	AAZ93525	Expansin gene sequ
27	313.4	31.6	824	21	AAC42473	Arabidopsis thalia
28	312.8	31.5	1213	22	AAD03711	Tomato seed expans
29	301.8	30.4	1293	21	AAC37064	Arabidopsis thalia
30	301.2	30.4	774	24	ABZ13037	Arabidopsis thalia
31	301.2	30.4	1037	21	AAC42618	Arabidopsis thalia
32	298.8	30.1	893	24	ABN98723	Arabidopsis thalia
33	298.6	30.1	1291	21	AAC50400	Arabidopsis thalia
34	287.6	29.0	475	21	AAZ93526	Expansin gene sequ
35	276.4	27.9	537	20	AAV68448	Melon expansin Cmb
36	270	27.2	410	25	ABX21914	Human GDP-mannose
37	264.8	26.7	1103	22	AAD03712	Tomato seed expans
38	262.6	26.5	727	17	AAT30255	Cotton fibre cell-
39	262.6	26.5	727	17	AAT13037	Cotton fibre speci
40	262.6	26.5	727	18	AAT70044	Cotton fibre speci
41	262.6	26.5	727	18	AAT62613	Cotton fibre speci
42	262.6	26.5	727	21	AAZ35549	cDNA sequence a co
43	256.6	25.9	2415	17	AAT30268	Cotton fibre clone
44	256.6	25.9	2415	17	AAT13053	Cotton fibre-speci
45	256.6	25.9	2415	18	AAT70039	Cotton B12 gene an

ALIGNMENTS

RESULT 1	ABA97161	standard; DNA; 684 BP.
ID	ABA97161	
XX	ABA97161;	
AC		
XX		
DT	19-APR-2002	(first entry)
XX		
DE	C. sativus DNA encoding SI expansin homologue.	
XX		
KW	Expansin; SI; cellulose-based textile; cotton; paper recycling;	
KW	paper pulp; plant tissue; papermaking; gene; cucumber; ds.	
XX		
OS	Cucumis sativus.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..684
FT		/*tag= a
FT		/partial
FT		/product= "SI expansin homologue"
FT		/note= "No start codon given"
XX		
PN	DE10032630-A1.	
XX		
PD	22-NOV-2001.	
XX		
PF	05-JUL-2000; 2000DE-1032630.	
XX		
PR	16-MAY-2000; 2000DE-1023561.	
XX		
PA	(FARB) BAYER AG.	

XX Berendes F, Rast HG, Vogt U, Gouloudis C;
XX WPI; 2002-155755/21.
DR P-PSDB; AAG80768.

for (DB) ref ready
us-09-383-506-9.rng
improve
Cibos

PT Vector encoding an expansin, useful in treatment of cellulosic
PT materials for paper recycling, providing large-scale production
XX
XX Claim 2; Page 11-14; 22pp; German.

XX This invention describes a novel vector (A) comprising (i) nucleic acid
CC (1) encoding an expansin (II) and (ii) coupled sequences that allow
CC expression of (I) in microorganisms. The recombinant expansins described
CC in the invention are used in preparation, treatment and finishing of
CC cellulose-based textiles (e.g. cotton) or in recycling of paper or for
CC preparation of pulp from plant tissue, as a substitute for corrosive
CC chemicals currently used in papermaking. Recombinant methods make
CC possible large scale production of extensins possible. This sequence
CC encodes the Cucumis sativus (cucumber) S1 extensin homologue described in
CC the invention.

XX Sequence 684 BP; 163 A; 179 C; 164 G; 178 T; 0 other;

Query Match 69.0%; Score 684; DB 24; Length 684;
Best Local Similarity 100.0%; Pred. No. 2e-184;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 GACTACGGTGGCTGGAGAGCGGCGCACCGCACCCTTTATAGTGTGGTGGAGCATGTGGC 282
DB 1 GACTACGGTGGCTGGAGAGCGGCGCACCGCACCCTTTATAGTGTGGTGGAGCATGTGGC 60

QY 283 ACCATGGGTGGAGCTGTGGGTATGGGAATTTATACAGCCCAAGGATAGGACGACGACG 342
DB 61 ACCATGGGTGGAGCTGTGGGTATGGGAATTTATACAGCCCAAGGATAGGACGACGACG 120

QY 343 GTGGCGCTGAGCATGCGCTATTATCAATGATGATGTTGTGCTGCTTGAATG 402
DB 121 GTGGCGCTGAGCATGCGCTATTATCAATGATGATGTTGTGCTGCTTGAATG 180

QY 403 ACTGTACAACAGACCCCTAAATGCTGCTCCGGGAATATTAGGCTCACTGCCACCAAC 462
DB 181 ACTGTACAACAGACCCCTAAATGCTGCTCCGGGAATATTAGGCTCACTGCCACCAAC 240

QY 463 TTTGGCCCTCTAATCTTGTCTCTCCCTAACAACAATGGTGGATGGTGAACCTCCTCTC 522
DB 241 TTTGGCCCTCTAATCTTGTCTCTCCCTAACAACAATGGTGGATGGTGAACCTCCTCTC 300

QY 523 CAACACTTCGACATGGCTGAGCCTGCTCTCTCAATCGCTCAATACCGAGCTGTATC 582
DB 301 CAACACTTCGACATGGCTGAGCCTGCTCTCTCAATCGCTCAATACCGAGCTGTATC 360

QY 583 GTCCCGCTCTCTTGTAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 642
DB 361 GTCCCGCTCTCTTGTAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420

QY 643 AATGGCCATCATCTTCAACCTGTTTGTATCACAACGTCGGTGGCGCAGGCGACGTC 702
DB 421 AATGGCCATCATCTTCAACCTGTTTGTATCACAACGTCGGTGGCGCAGGCGACGTC 480

QY 703 CACTCTGTGTGATTAAGGGGTCTGCAACTGATGGCAATCCATGTCTAGAAATTTGGGCG 762
DB 481 CACTCTGTGTGATTAAGGGGTCTGCAACTGATGGCAATCCATGTCTAGAAATTTGGGCG 540

QY 763 CAAAACCTGGCAAGCAACAATCTATCTCAATGGCCAGGCTTCTTCAAGTCACTCTT 822
DB 541 CAAAACCTGGCAAGCAACAATCTATCTCAATGGCCAGGCTTCTTCAAGTCACTCTT 600

QY 823 AGTATGGTGGCACTGCTCACTGCTATTAATCTGTTCTTCAATTTGGCAATTTGGGCG 882
DB 601 AGTATGGTGGCACTGCTCACTGCTATTAATCTGTTCTTCAATTTGGCAATTTGGGCG 660
QY 883 ACCTATGAAGGCCCTCAATTCTAA 906

DB 661 ACCTATGAAGGCCCTCAATTCTAA 684

RESULT 2
AAT13320

ID AAT13320 standard; DNA; 681 BP.
XX
AC AAT13320;

DT 25-MAR-2003 (updated)
DT 08-JUL-1996 (first entry)
XX
DE Cucumber expansin-29 cDNA.

XX Expansin-29; plant cell wall; cellulose; paper recycling; de-linking;
XX polysaccharide; cucumber; ss.

XX Cucumis sativus var. Burpee Pickler.

XX AU9540262-A.

XX 04-APR-1996.

XX 06-DEC-1995; 95AU-0040262.

XX 12-MAY-1993; 93US-0060944.

XX 12-MAY-1995; 95US-0440517.

XX 12-MAY-1994; 94AU-0068320.

XX (PENN-) PENN STATE RES FOUND.

XX Cosgrove DJ, McQueen-Mason S;

XX WPI; 1996-201150/21.

XX P-PSDB; AAR94527.

XX Expansin proteins which alter the mechanical strength of
XX poly:saccharide(s) - useful in paper mfr. and recycling

XX Disclosure; Page 30; 60pp; English.

XX A cDNA clone (AAT13320) codes for cucumber expansin-29 (AAR94527),
XX a member of a novel class of proteins that catalyse the extension of
XX plant cell walls and the weakening of the hydrogen bonds in pure
XX cellulose. It was obt. by PCR amplification of cucumber seedling
XX cDNA using primers based on isolated peptide fragments of the protein.

XX The gene can be expressed in bacterial or other systems for use in
XX recombinant expansin prodn. Expression of the gene in transgenic
XX plants may allow alteration of plant growth characteristics,
XX while expression in plant tissue cultures may allow improved prodn.

XX of useful chemicals.

XX (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 681 BP; 161 A; 179 C; 164 G; 177 T; 0 other;

Query Match 68.6%; Score 681; DB 17; Length 681;
Best Local Similarity 100.0%; Pred. No. 1.4e-183;
Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 GACTACGGTGGCTGGAGAGCGGCGCACCGCACCCTTTATAGTGTGGTGGAGCATGTGGC 282
DB 1 GACTACGGTGGCTGGAGAGCGGCGCACCGCACCCTTTATAGTGTGGTGGAGCATGTGGC 60

QY 283 ACCATGGGTGGAGCTGTGGGTATGGGAATTTATACAGCCCAAGGATAGGACGACGACG 342
DB 61 ACCATGGGTGGAGCTGTGGGTATGGGAATTTATACAGCCCAAGGATAGGACGACGACG 120

QY 343 GTGGCGCTGAGCATGCGCTATTATCAATGATGATGATGATGATGATGATGATGATGATGATGATG 402
DB 121 GTGGCGCTGAGCATGCGCTATTATCAATGATGATGATGATGATGATGATGATGATGATGATGATG 180

QY 403 ACTTGATCAAAACGACCCCTAAATGTCCTTCCGGAACTATTAGGGTCACTGCCAAC 462
DB 181 ACTTGATCAAAACGACCCCTAAATGTCCTTCCGGAACTATTAGGGTCACTGCCAAC 240
QY 463 TTTTGCCCTCCTAATTGCTCTCCCTAACAACAATGATGGATGGCAACCTCTCTC 522
DB 241 TTTTGCCCTCCTAATTGCTCTCCCTAACAACAATGATGGATGGCAACCTCTCTC 300
QY 523 CAACACTTGACATGGCTGAGCGCTCTCTCAATGCTCAATACCGAGCTGTATC 582
DB 301 CAACACTTGACATGGCTGAGCGCTCTCTCAATGCTCAATACCGAGCTGTATC 360
QY 583 GTCCCGCTCTCTTCTGTAGGGTACATGATGAGAAGGAGTGAGTTTACAATC 642
DB 361 GTCCCGCTCTCTTCTGTAGGGTACATGATGAGAAGGAGTGAGTTTACAATC 420
QY 643 AATGGCCACTCACTTCAACCTGTTTGTATCAAAACGTCGGTGGCCGACGCGTC 702
DB 421 AATGGCCACTCACTTCAACCTGTTTGTATCAAAACGTCGGTGGCCGACGCGTC 480
QY 703 CACTCTGTGTGATTAAGGGGTCTGCACTGATGGCAATCCATGTCTAGAAATTGGGGC 762
DB 481 CACTCTGTGTGATTAAGGGGTCTGCACTGATGGCAATCCATGTCTAGAAATTGGGGC 540
QY 763 CAAAACTGGCAAGCAACAACATCTCAATGGCCAGGCTTCTTCAAGTCACTCTT 822
DB 541 CAAAACTGGCAAGCAACAACATCTCAATGGCCAGGCTTCTTCAAGTCACTCTT 600
QY 823 AGTGATGGTGGCACTCTCACTGCTATATCTGCTCTTCCAAATTGGCAATTGGCCAA 882
DB 601 AGTGATGGTGGCACTCTCACTGCTATATCTGCTCTTCCAAATTGGCAATTGGCCAA 660
QY 883 ACCTATGAAGGCCCTCAATTC 903
DB 661 ACCTATGAAGGCCCTCAATTC 681

RESULT 3
ABA97162 standard; DNA; 681 BP.

AC ABA97162;

DT 19-APR-2002 (first entry)

DE C. sativus DNA encoding expansin csepla.

KW Expansin; cellulose-based textile; cotton; paper recycling; csepla;
paper pulp; plant tissue; papermaking; gene; cucumber; ds.

OS Cucumis sativus.

FH Key Location/Qualifiers
FT CDS 1.681
FT /*tag= a
FT /partial
FT /product= "csepla"
FT /note= "No start or stop codon given"

PN DE10032630-A1.

PD 22-NOV-2001.

PF 05-JUL-2000; 2000DE-1032630.

PR 16-MAY-2000; 2000DE-1023561.

PA (FARB) BAYER AG.

PI Berendes F, Raat HG, Vogt U, Gouloudis C;

DR WPI; 2002-155755/21.

DR P-PSDB; AAG80769.

XX Vector encoding an expansin, useful in treatment of cellulosic
PT materials for paper recycling, providing large-scale production
XX
PS Claim 2; Page 14-16; 22pp; German.
XX
CC This invention describes a novel vector (A) comprising (i) nucleic acid
CC (II) encoding an expansin (II) and (ii) coupled sequences that allow
CC expression of (I) in microorganisms. The recombinant expansin described
CC in the invention are used in preparation, treatment and finishing of
CC cellulose-based textiles (e.g. cotton) or in recycling of paper or for
CC preparation of pulp from plant tissue, as a substitute for corrosive
CC chemicals currently used in papermaking. Recombinant methods make
CC possible large scale production of extensins possible. This sequence
CC encodes the Cucumis sativus (cucumber) extensin, csepla, described in
CC the invention.
XX
SQ Sequence 681 BP; 161 A; 178 C; 164 G; 178 T; 0 other;

Query Match 68.2%; Score 676.2; DB 24; Length 681;
Best Local Similarity 99.6%; Pred. No. 3.3e-182;
Matches 678; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 223 GACTACGGTGGCTGGCAGAGCGGCACGCACTTTTATGAGTGGTGACGCACTGGC 282
DB 1 GACTACGGTGGCTGGCAGAGCGGCACGCACTTTTATGAGTGGTGACGCACTGGC 60
QY 283 ACCATGGGTGAGCTTGTGGGTATGGAATTATACAGCAAGGGTATGGCAAGACAG 342
DB 61 ACCATGGGTGAGCTTGTGGGTATGGAATTATACAGCAAGGGTATGGCAAGACAG 120
QY 343 GTGGCGCTGAGCACTGGCTATTTAACAATGATTAAGTTGGTGTCTTGAATG 402
DB 121 GTGGCGCTGAGCACTGGCTATTTAACAATGATTAAGTTGGTGTCTTGAATG 180
QY 403 ACTGTACAAGCAAGCCCTAATAGTGCCTCCGGGAATTAAGGTCACTGCCAAC 462
DB 181 ACTGTACAAGCAAGCCCTAATAGTGCCTCCGGGAATTAAGGTCACTGCCAAC 240
QY 463 TTTTGCCCTCCTAATTGCTCTCCCTAACAACAATGATGGATGGCAACCTCTCTC 522
DB 241 TTTTGCCCTCCTAATTGCTCTCCCTAACAACAATGATGGATGGCAACCTCTCTC 300
QY 523 CAACACTTGACATGGCTGAGCGCTCTCTCAATGCTCAATACCGAGCTGTATC 582
DB 301 CAACACTTGACATGGCTGAGCGCTCTCTCAATGCTCAATACCGAGCTGTATC 360
QY 583 GTCCCGCTCTCTTCTGTAGGGTACATGATGAGAAGGAGTGAGTTTACAATC 642
DB 361 GTCCCGCTCTCTTCTGTAGGGTACATGATGAGAAGGAGTGAGTTTACAATC 420
QY 643 AATGGCCACTCACTTCAACCTGTTTGTATCAAAACGTCGGTGGCCGACGCGTC 702
DB 421 AATGGCCACTCACTTCAACCTGTTTGTATCAAAACGTCGGTGGCCGACGCGTC 480
QY 703 CACTCTGTGTGATTAAGGGGTCTGAACTGGATGGCAATCATGTCTAGAAATTGGGGC 762
DB 481 CACTCTGTGTGATTAAGGGGTCTGAACTGGATGGCAATCATGTCTAGAAATTGGGGC 540
QY 763 CAAAACTGGCAAGCAACAACATCTCAATGGCCAGGCTTCTTCAAGTCACTCTT 822
DB 541 CAAAACTGGCAAGCAACAACATCTCAATGGCCAGGCTTCTTCAAGTCACTCTT 600
QY 823 AGTGATGGTGGCACTCTCACTGCTATATCTGCTCTTCCAAATTGGCAATTGGCCAA 882
DB 601 AGTGATGGTGGCACTCTCACTGCTATATCTGCTCTTCCAAATTGGCAATTGGCCAA 660
QY 883 ACCTATGAAGGCCCTCAATTC 903
DB 661 ACCTATGAAGGCCCTCAATTC 681

RESULT 4

ID	Accession	Standard	CDNA	BP
AD32964	AD32964	standard	CDNA	1144 BP
AC	AD32964			
DT	01-JUL-2002	(first entry)		
DE	Pear expansin 2 (Exp2)	CDNA		
XX	Pear; cell wall hydrolase; beta-galactosidase; pectin methyltransferase; PME; beta-gal; polygalacturonase; PG; expansin1; Exp1; expansin2; Exp2; fruit ripening; gene expression; transgenic plant; transgenic; enzyme; gene; ss.			
OS	Pyrus communis.			
FH	Key	Location/Qualifiers		
FT	CDS	83..340		
FT		/*tag= a		
FT		/product= "Pear expansin 2 protein #2"		
FT	CDS	83..850		
FT		/*tag= a		
FT		/product= "Pear expansin 2 protein #1"		
FT		/transl_except= (pos:335..343, aa:Leu-Asn)		
FT		/transl_except= (pos:353..361, aa:Gln-Pro)		
FT		/transl_except= (pos:413..421, aa:Ser-Leu)		
FT		/transl_except= (pos:479..487, aa:Gly-Ala)		
FT		/transl_except= (pos:767..775, aa:Gln-Arg)		
FT		/transl_except= (pos:773..781, aa:Arg-Asn)		
FT		/transl_except= (pos:806..814, aa:Trp-Leu)		
FT		/note= "All the translational exceptions comprise an in-frame stop codon; CDS does not include stop codon"/partial		
PN	WO200216613-A2.			
PD	28-FEB-2002.			
PF	20-AUG-2001; 2001WO-PT00021.			
PR	22-AUG-2000; 2000PT-0102511.			
PA	(ICAT-) ICAT INST CIENCIA APLICADA E TECNOLOGIA.			
PI	Matias Fonseca SC, Balde A, Soares Pais MS;			
XX	WPI; 2002-280942/32.			
DR	P-PSDB; AAE20571, AAE20578.			
PT	New beta-galactosidase, pectin methyltransferase, polygalacturonase, expansin1, and expansin2 proteins and nucleic acids, useful for regulating fruit ripening or creating transgenic plants			
PS	Claim 14; Page 38-39; 45pp; English.			
XX	The present invention relates to novel genes which encode cell wall hydrolases such as beta-galactosidase (beta-Gal), pectin methyltransferase (PME), polygalacturonase (PG) and cell wall proteins such as expansin1 (Exp1) and expansin2 (Exp2) proteins from pear fruit. The nucleic acids are useful for regulating fruit ripening and for suppressing endogenous beta-Gal, PME, PG, Exp1 and Exp2 genes in any fruit or other plant organs, thus modifying the structure of the cell walls of the fruit or plant and providing for ripe yet firm fruit and vegetables. The genes may be used to screen a cDNA library or a genomic library from any species, to inhibit or enhance gene expression or to produce transgenic plants. The present sequence is a cDNA encoding pear expansin 2 protein.			
XX	Sequence 1144 BP; 325 A; 258 C; 242 G; 319 T; 0 other;			
XX	Query Match	40.8%; Score 404.4; DB 24; Length 1144;		
XX	Best Local Similarity	73.9%; Pred. No. 1e-104;		
XX	Matches 553; Conservative	0; Mismatches 191; Indels 4; Gaps 3;		

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RESULT 6
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AAC40777;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 29509.

KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

PN EP1033405-A2.

XX PD 06-SEP-2000.

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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 65548.
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
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QY 279 TGGCACCATTGGGTGGAGCTTGTGGGTATGGAAATTATACAGCCAAAGGTATGGCAGAA 338
DB 150 CGGCACAATGGGTGGTGGCTTGTGGATATGGTAACTATATAGCCAAAGGCTACGGCAGAG 209
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AC AAC33521;
XX 17-OCT-2000 (first entry)
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XX DE Hybridisation assay; genetic mapping; gene expression control;
XX KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.

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PD 06-SEP-2000.
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PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

Query Match 38.1%; Score 377.8; DB 21; Length 1198;
Best Local Similarity 72.0%; Pred. No. 3.9e-97;
Matches 493; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY	219	CGCTGACTACGGTGGCTGGCAGAGCGGCGACGCCACCTTTATGTTGGTGACGCATC	278
Db	115	CGGCTACGGTGGCGTTGATCAACGCTACGCCACTTTTACGTTGGTGATGCTTC	174
QY	279	TGGCACCATGGGTGAGCTTGTGGTATGGGAATTATACAGCCAAAGGATGACAGAA	338
Db	175	CGGCACATGGGTGGTGTGATATGTAATCTATATAGCCAAAGGCTACGGACGAG	234
QY	339	CACGGTGGCTGAGCACTGGCTATTTAACAATGATTAAGTTGTGCTTGTTCGA	398
Db	235	CACGGCGCTTAAGCACAGCTCTTTCACAATGACTAGCTGTGTTCTTGTTCGA	294
QY	399	AATGACTTGTACAACGACCCCTAATGTGCTTCCGGGAATATTAGGTCACCTGCCAC	458
Db	295	GATAAGATGTGAAAACGATGTAATGTGTTTACCTGGCTCAATCGTTTAACCGCTAC	354
QY	459	CAACTTTTGCCCTCCTAATTGCTCTCCCTTACAACAATGTGATGTCACACCTTC	518
Db	355	AACTTCTGCCCCGCCAAATAACGCGTTAGCGAACAATAATGGCGTGTGTAATCCTCC	414
QY	519	TCTCCACACTTGCACATGGCTGAGCCCTTCCCTTCAAATCGCTCAATACCGAGCTGG	578
Db	415	TCTTGAACACTTTGACCTTGCTCAGCCCTGTTTTCACCGCAITTGCTCAGTACAGAGCTGG	474
QY	579	TATCGTCCCGTCTCTTTTCGTAGGGTACCATGTATGAAGAAAGGTGAGTGAAGTTTAC	638

Db	475	AATCGTCCCTGTTTCCTACAGAAAGGTTCCCTTGACAGAGAGAGAAATTAAGATTAC	534
QY	639	AATCAATGGCCACTCATACTTCAACTCTGTTTGTATCACAACGTCGTGGCGCAGCGA	698
Db	535	GATAAAGCGCACATCACTTCAACTTGTGTGATCACAACGTCGTGGTCGGAGA	594
QY	699	CGTCCACTCTGTGTCGATAAAGGGTCTCGAATGATGCAATTCATGTCTAAGAAATTG	758
Db	595	CGTTCACCTCGCGCGCATCAAGGTTCAAGAACGTCGTGCAAGCTATGTCAAGAACTG	654
QY	759	GGGCCAAAACCTGGCAAGCAACATATCTCAATGCGCAAGGCTTTCCTTCAAGTCAC	818
Db	655	GGGCAAAATTGGCAAGCAACTCTTACCTCAACGGTCAAGCACTTCCCTTAAGTCAAC	714
QY	819	TCTTAGTATGTGTCGCACTCTCACTGCTATATACTGTTCCCTTCCAAATTGCAATTGG	878
Db	715	CACGACGACGGCGGCACAGTTGTCTCCTTCAACGCCGCTCCTGCGGCTGTTATAGG	774
QY	879	CCAAACCTATGAAGGCCCTCAATTC	903
Db	775	CCAGACTTTTGCCGGTGGACAGTTC	799

RESULT 10
AAC50633
ID AAC50633 standard; DNA; 1233 BP.

XX	AAC50633;	
XX	18-OCT-2000	(first entry)
XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 65567.	
XX	Hybridisation assay; genetic mapping; gene expression control;	
XX	protein identification; signal transduction pathway;	
XX	metabolic pathway; promoter; termination sequence; ss.	
XX	Arabidopsis thaliana.	
PN	EP1033405-A2.	
XX	06-SEP-2000.	
XX	25-FEB-2000;	2000EP-0301439.
PF	25-FEB-1999;	99US-0121825.
XX	05-MAR-1999;	99US-0123180.
PR	09-MAR-1999;	99US-0123548.
PR	23-MAR-1999;	99US-0125788.
PR	25-MAR-1999;	99US-0126264.
PR	29-MAR-1999;	99US-0126785.
PR	01-APR-1999;	99US-0127462.
PR	06-APR-1999;	99US-0128234.
PR	08-APR-1999;	99US-0128714.
PR	16-APR-1999;	99US-0129845.
PR	19-APR-1999;	99US-0130077.
PR	21-APR-1999;	99US-0130449.
PR	23-APR-1999;	99US-0130510.
PR	23-APR-1999;	99US-0130891.
PR	28-APR-1999;	99US-0131449.
PR	30-APR-1999;	99US-0132048.
PR	30-APR-1999;	99US-0132407.
PR	04-MAY-1999;	99US-0132484.
PR	05-MAY-1999;	99US-0132485.
PR	06-MAY-1999;	99US-0132486.
PR	06-MAY-1999;	99US-0132487.
PR	07-MAY-1999;	99US-0132863.
PR	11-MAY-1999;	99US-0134256.
PR	14-MAY-1999;	99US-0134218.
PR	14-MAY-1999;	99US-0134219.
PR	14-MAY-1999;	99US-0134221.
PR	14-MAY-1999;	99US-0134370.

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PR 21-MAY-1999; 99US-0135353.
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PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
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PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
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PR 27-JUL-1999; 99US-0145918.

PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
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PR 05-AUG-1999; 99US-0147260.
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PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148319.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
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PR 17-AUG-1999; 99US-0149175.
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PR 23-AUG-1999; 99US-0149902.
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PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
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PR 31-AUG-1999; 99US-0151438.
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PR 10-SEP-1999; 99US-0153070.
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PR 16-JUL-1999; 99US-0144085.
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PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.

PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
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PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
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PR 22-OCT-1999; 99US-0160980.
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PR 25-OCT-1999; 99US-0161404.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 37.0%; Score 366.8; DB 21; Length 1236;
Best Local Similarity 71.9%; Pred. No. 5.4e-94;
Matches 493; Conservative 0; Mismatches 192; Indels 1; Gaps 1;

QY 219 CGCTGACTACCGGTGGCTGGCAGAGCGGCCACCCACTTTATGTGTGGTGAACGCATC 278
DB 155 CGTCTACCGGTGGCGGTGGATCAACGCTCAGCCACTTTTACGGTGTGTGATGCTTC 214
QY 279 TGGCACCATGGGTGAGGCTTGTGGTATGGAAATTATACAGCCCAAGGGTATGGCAGAA 338
DB 215 CGGCACAATGGGTGTGCTTGTGGATATGTAATCTATATAGCCCAAGGCTACGGGACGAG 274
QY 339 CACGGTGGCGCTGAGCACTG-CGCTATTTAACAATGATTAAGTGTGTGCTTGCCTTCG 397
DB 275 CACGGCGGCTTAAGCACAGSCTCTCTCAACAATGACTTAAGCTGTGTCTTGCCTTGG 334
QY 398 AATGACTGTACAAACGACCCCTAATGTGCTTCCGGAACTATTAGGCTCACTGCCA 457
DB 335 AGATAAGATGTGAACACGATGTAAATGTGTATTACCTGGCTCAATCGTTGAACCGCTA 394
QY 458 CCAACTTTGGCCCTCTTAATTGCTCTGCTTAACAACAATGTGTGATGTGCAACCCCTC 517
DB 395 CAAACTTGTGCCCCGCCAAATTAACGCGTTAGCGAACAATAATGCGGTTGTGTAATCCTC 454
QY 518 CTCTCCAACACTTGACATGGCTGAGCTGCTTCCCTTGAATGCTCAATACCGAGCTG 577
DB 455 CTCTGAACACTTGAACCTTGTCTCAGCGCTGTGTTTTCACGCAATGTCTCAGTACAGAGCTG 514

QY	578	GTATCGTCCCCGCTCCTTTCGTAGGGTACCATGTATGAAGAAAGGTGAGTGAAGTTTA	637
Db	515	GAATCGTCCCTGTTCCTACAGAAAGGTTCTTGACGAGAAAGAGAAATAAGATTCA	574
QY	638	CAATCAATGGCCACTCATCTTCAACCTCGTTTGTATCAAAACGTGGTGGCGACGGC	697
Db	575	CGATAAACGGCCACTCATCTTCAACCTTGTGCTGATCAAAACGTGGTGGTCCGGAG	634
QY	698	ACGTCACTCTGTGTCGATAAAGGGTTCGAACCTGATGGCAATCCATGCTAGAAATT	757
Db	635	ACGTCACTCGGGCGGCATCAAGGTTCAAGAACAGTGTGGCAAGTATGTCAAGAACT	694
QY	758	GGGGCCAAAACGTGGCAAAAGCAACAATACTCAATGGCCAGGCTTTCTTCAAGTCA	817
Db	695	GGGGGCAAAATTGGCAAAAGCAACTCTTACTCAACGGTCAAGCACTTTCTTAAGTCA	754
QY	818	CTCTAGTGTATGTCGCACTCTCACTGCGCTATAATCTCGTTCTTCCAATTGGCAATTTG	877
Db	755	CCACCAAGCAGCGCGCCGACAGTGTCTCTTCAACGCCGCTCTGCCGGCTGCTTATG	814
QY	878	GCCAAACCTATGAAGGCCCTCAATTC	903
Db	815	GCCAGACTTTTGCCGGTGAACAGTTTC	840

RESULT 12	
ID ABA97164	standard; DNA; 687 BP.
XX AC ABA97164;	
XX DT 19-APR-2002	(first entry)
XX DE N. tabacum DNA encoding expansin nexp4a.	
XX KM Expansin; cellulose-based textile; cotton; paper recycling; csexpla;	
XX XW paper pulp; plant tissue; papermaking; gene; tobacco; ds.	
XX OS Nicotiana tabacum.	
XX FH Key Location/Qualifiers	
FT CDS 1..687	
FT /*tag= a	
FT /partial	
FT /product= "nexp4a"	
FT /note= "No start or stop codon disclosed"	
XX PN DE10032630-A1.	
XX PD 22-NOV-2001.	
XX PF 05-JUL-2000; 2000DE-1032630.	
XX PR 16-MAY-2000; 2000DE-1023561.	
XX PA (FARB) BAYER AG.	
XX PI Berendes F, Rast HG, Vogt U, Gouloudis C;	
XX DR WPI; 2002-155755/21.	
XX DR P-PADB; AAG80771.	
XX PT Vector encoding an expansin, useful in treatment of cellulosic	
PT materials for paper recycling, providing large-scale production -	
PS Claim 2; Page 19-21; 22pp; German.	
XX CC This invention describes a novel vector (A) comprising (i) nucleic acid	
CC (1) encoding an expansin (II) and (ii) coupled sequences that allow	
CC expression of (I) in microorganisms. The recombinant expansins described	
CC in the invention are used in preparation, treatment and finishing of	
CC cellulose-based textiles (e.g. cotton) or in recycling of paper or for	
CC preparation of pulp from plant tissue, as a substitute for corrosive	

CC chemicals currently used in papermaking. Recombinant methods make
CC possible large scale production of extensins possible. This sequence
CC encodes the lycopersicon esculentum (tomacco) extensin, described
CC in the invention.
XX
SQ Sequence 687 BP; 183 A; 128 C; 170 G; 206 T; 0 other;

Query Match	36.5%;	Score 361.8;	DB 24;	Length 687;
Best Local Similarity	70.9%;	Pred. No. 1.1e-92;		
Matches 480; Conservative	0;	Mismatches 197;	Indels 0;	Gaps 0;

QY	229	GGTGGCTGGCAGACGGCCACCGCACCTTTATGSGTGGTGAGCCATCTGGCACCATG	288
	10	GGAGGTTGGATTAAATGCTCATGCTACCTTTATGSGTGGTGAGTGCCTCTGGCACAATG	69
QY	289	GGTGGAGCTTGIGGGTATGGGAATTTATACAGCCAAAGGGTATGGCAGAAACGGTGGCG	348
	70	GGTGGGGCATGTGATATGGAAATTTGTATAGCCAAAGGGTATGGTACAAATACTGCAGCA	129
QY	349	CTGAGCACTGCGCTATTTAACAAATGATTAAATGTTGTTGCTGCTTCCAAATGACTTGT	408
	130	TTAAGTACAGCTATGTTCAACAATGGGTTGAGCTGTGGTCTTGTGTTTGGATTAAGTGT	189
QY	409	ACAAACGACCCTAAATGTTGCTCCCGGAACCTAATTAAGGTCACAGCCCAACTTTGC	468
	190	GTGATGATAGGAAGGGTGTGGCTGTTCAATGTGTGCACAGCTAACCAATTTTGC	249
QY	469	CTTCCTAATTGCTCTCCCTAACAAACATGTTGATGTTGCAACCTCTCTCCAAC	528
	250	CCACCAATAATGATGCTGCTTAACAATGACAGGGGTTGGTAAATCTCCCTTCACAT	309
QY	529	TTGCACATGCGTGAACCTGCTTCCAATCGCTCAATACCGAGCTGATGCTCCC	588
	310	TTTGATCTCTCTGACGCTATTTTCCAACACATTTGCTCAATACAAAGCTGAATGTTCT	369
QY	589	GTCTCCTTTCGTAGGGTACCATGTATGAAGAAAGTGGAGTGAGTTTCAATCAATGGC	648
	370	GTGCTTACAGAGGGTACCCTGCAGAGAGGAGTATAAGTTCAACATCAATGGA	429
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AC ABZ12286;
XX
DT 21-JAN-2003 (first entry)
XX
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 91.
XX
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds
XX
OS Arabidopsis thaliana.

XX WO200216655-A2.
 PN
 XX
 PD 28-FEB-2002.
 XX
 PF 24-AUG-2001; 2001WO-US26685.
 XX
 PR 24-AUG-2000; 2000US-227866P.
 PR 26-JAN-2001; 2001US-264647P.
 PR 22-JUN-2001; 2001US-300111P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 PI Harper JF, Kreps J, Wang X, Zhu T;
 XX WPI; 2002-304127/34.
 DR
 PT Identifying a stress condition to which a plant cell has been exposed
 PT and producing plants with increased tolerance to these abiotic stresses
 PT
 PS Claim 144; SEQ ID NO 91; 577pp + Sequence Listing; English.
 XX
 CC The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising:
 CC (a) contacting nucleic acid representative of expressed polynucleotides
 CC in the plant cell with an array or probes representative of the plant
 CC cell genome; and
 CC (b) detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
 CC in methods of the invention.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied to Derwent by
 CC the European Patent Office.
 XX
 SQ Sequence 753 BP; 196 A; 187 C; 187 G; 183 T; 0 other;
 Query Match 36.4%; Score 360.6; DB 24; Length 753;
 Best Local Similarity 71.1%; Pred. No. 2.5e-92;
 Matches 477; Conservative 0; Mismatches 194; Indels 0; Gaps 0;
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XX AC AB213264;
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DT 21-JAN-2003 (first entry)

XX Arabidopsis thaliana stress regulated gene SEQ ID NO 1069.

XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX Arabidopsis thaliana.

OS WO200216655-A2.

PN 28-FEB-2002.

PD 24-AUG-2001; 2001WO-US26685.

PF 24-AUG-2000; 2000US-227866P.

PR 26-JAN-2001; 2001US-264647P.

PR 22-JUN-2001; 2001US-300111P.

XX (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 PI Harper JF, Kreps J, Wang X, Zhu T;

XX WPI; 2002-304127/34.

PT Identifying a stress condition to which a plant cell has been exposed
 PT and producing plants with increased tolerance to these abiotic stresses
 PT

PS Claim 144; SEQ ID NO 1069; 577pp + Sequence Listing; English.

XX The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising:
 CC (a) contacting nucleic acid representative of expressed polynucleotides
 CC in the plant cell with an array or probes representative of the plant
 CC cell genome; and
 CC (b) detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
 CC in methods of the invention.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied to Derwent by
 CC the European Patent Office.
 XX

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QY	842	CTGCTATATCTCGTTCCTTCCAAATGGCAATTTGGCCAAACCTATGAAGCCCTCAAT	901
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QY	902	TC 903	
Db	841	TC 842	

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 Job time : 317 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2003, 21:57:27 ; Search time 362 Seconds
(without alignments)
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Searched: 221978 seqs, 1666101734 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	681	68.6	681	10	US-09-896-301-1 Sequence 1, Appli
2	394.2	39.7	762	10	US-09-938-842A-1088 Sequence 1088, Ap
3	386.2	38.9	1153	13	US-10-150-559-3 Sequence 3, Appli
4	373.8	37.7	759	13	US-10-409-701-8 Sequence 8, Appli
5	360.6	36.4	747	10	US-09-938-842A-91 Sequence 91, Appl
6	360.4	36.3	743	10	US-09-938-842A-1069 Sequence 1069, Ap
7	341.6	34.4	774	10	US-09-938-842A-89 Sequence 89, Appl
8	301.2	30.4	774	10	US-09-938-842A-842 Sequence 842, Appl
c	298.8	30.1	893	9	US-09-770-445-491 Sequence 491, App
10	270	27.2	410	10	US-09-878-574-3973 Sequence 3973, Ap
11	251.2	25.3	768	10	US-09-938-842A-1046 Sequence 1046, Ap
12	251	25.3	391	10	US-09-878-574-62 Sequence 62, Appl
13	169.2	17.1	366	9	US-09-770-791-430 Sequence 430, App
14	149	15.0	373	10	US-09-878-574-3468 Sequence 3468, Ap
15	148.6	15.0	391	10	US-09-878-574-1206 Sequence 1206, Ap

16	92.6	9.3	293	9	US-09-294-093B-2002	Sequence 2002, Ap
17	90	9.1	394	10	US-09-878-574-2728	Sequence 2728, Ap
18	88.8	9.0	262	10	US-09-878-574-14926	Sequence 14926, A
19	80.8	8.1	285	10	US-09-878-574-13697	Sequence 13697, A
20	73.4	7.4	259	10	US-09-878-574-12313	Sequence 12313, A
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22	48.6	4.9	238	9	US-09-294-093B-4389	Sequence 4389, Ap
c	48	4.8	5586	13	US-10-311-455-621	Sequence 621, App
c	47.4	4.8	380	9	US-09-770-791-183	Sequence 183, App
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c	42.4	4.3	5455	13	US-10-204-708-34	Sequence 34, Appl
c	42.4	4.3	3673778	13	US-10-312-841-2	Sequence 2, Appli
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c	41.8	4.2	903	13	US-10-029-386-20462	Sequence 20462, A

ALIGNMENTS

RESULT 1
US-09-896-301-1
; Sequence 1, Application US/09896301
; Patent No. US20020103355A1
; GENERAL INFORMATION:
; APPLICANT: Cosgrove, Daniel J
; APPLICANT: McQueen-Mason, Simon
; APPLICANT: Gullitnan, Mark J
; APPLICANT: Shcherban, Tatyana
; APPLICANT: Shi, Jun
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; FILE REFERENCE: 1194/1C114US3
; CURRENT APPLICATION NUMBER: US/09/896,301
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/092,160
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 08/440,517
; PRIOR FILING DATE: 1995-05-12
; PRIOR APPLICATION NUMBER: 08/242,090
; PRIOR FILING DATE: 1994-05-12
; PRIOR APPLICATION NUMBER: 08/060,944
; PRIOR FILING DATE: 1993-05-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA cucumber
; OTHER INFORMATION: expansin
US-09-896-301-1

Query Match 68.6%; Score 681; DB 10; Length 681;
Best Local Similarity 100.0%; Pred. No. 2.8e-188;
Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2

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; US-09-938-842A-1088
; Sequence 1088, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR APPLICATION NUMBER: US 2001-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/300,111
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1088
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

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US-09-938-842A-1088

Query Match 39.7%; Score 394.2; DB 10; Length 762;
 Best Local Similarity 73.1%; Pred. No. 1.8e-104;
 Matches 520; Conservative 0; Mismatches 188; Indels 3; Gaps 1;

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; Sequence 3, Application US/10150559
; Publication No. US20030221218A1
; GENERAL INFORMATION:
; APPLICANT: Wilkins, Thea A.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Bioengineering Cotton Fiber Properties
; FILE REFERENCE: 023070-116500US
; CURRENT APPLICATION NUMBER: US/10/150,559
; PRIOR FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:

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OTHER INFORMATION: expansion
US-10-150-559-3

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Db	237	GTCAAAGGGTATGGAACGAGCACAGCACTTTGAGCACTTGCACTTTTCAACAATGGCTTGA	296
QY	380	GTTGTGTGTCTTGCTTCGAATGACTTGTACAAACGACCTAAATGTGCTTCCGGAA	439
Db	297	GCTGCGGTGCTTCTTACGAGCTCCGGTGCACAATGATCTCAATGGTGCAATTAGTCGA	356
QY	440	CTATTAGGGTCACTGCCACCAACTTTTGCCCTCCTAACTTTGCTCTCCCTAACAACAATG	499
Db	357	CCATTAACCGTGACAGCCACCAACTTTGTCCCTTAATATGCTTATCTAGTGACAAATG	416
QY	500	GTEGATGTGTGCAACCTCTCTCTCCACACACTTGACATGGCTGAGCCTGCTTCTTCAA	559
Db	417	GCGGGTGTGCAATCCCCACGAGAACACTTGTATTGGCCGAACCGGCACTTCTTGAGA	476
QY	560	TGCTCAATACCGAGCTGGTATCGTCCCGTCTCCTTTCGTAGGGTACCATGTATGAAGA	619
Db	477	TGCGGAATATCGAGCTGGGATCGTCCCTGTTATGTTCAAGAAGGTGTGATGAAGA	536
QY	620	AAGGTGAGTGAAGTTTACAATCAATGGCCACTCATACTTCAACCTCGTTTGATCACA	679
Db	537	AAGGAGGCATCAGGTACACCATGAATGGACATTCGTACTTCAACATGGTGTGATAACA	596
QY	680	ACGTGCGTGGCGCAGCGACGTCACTCTGTGTGATAAAGGGGTCTCGAAGTGGATGGC	739
Db	597	ACGTGGAGGGCGAGGGGATATAACGTCAAGTGTCAATCAAGGTTCCAAAACAGATGGC	656
QY	740	AATTCATGTCTAGAAATTTGGGGCCAAACTGGCAAGCAACAACACTATCTCAATGGCCAG	799
Db	657	TACCTATGTCCAGAAATTTGGGGCCAAAACCTGGCAGAGCAATGCTTAACTTAACGGCCAA	716
QY	800	GCCCTTCTTTCAAGTCACTCTTAGTGATGGTGCACCTCTCACTGCTTAATCTCGTTC	859
Db	717	GCTCTCTTTTCAAGTGAAGTCCAGCGATAGCAGGACTATCACAAACTCAATGTAGTGC	776
QY	860	CTTCCAAATGGCAATTTGGCCAAACCTATGAAGGCCCTCAATTTCTAAACA 910	
Db	777	CCGCTGCTTGGCAATTCGACAAACTTTTGAAGGAGGCCAGTTTAAAGACA 827	

RESULT 4
US-10-409-701-8

```

; Sequence 8, Application US/10409701
; Publication No. US20030221224A1
; GENERAL INFORMATION:
; APPLICANT: Zinselmeyer, Chris
; APPLICANT: Helentjaris, Timothy G.
; TITLE OF INVENTION: Enhanced Silk Exsertion Under Stress
; FILE REFERENCE: 1421
; CURRENT APPLICATION NUMBER: US/10/409,701
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,796
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 8
;
; LENGTH: 759
;

```

```

; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (759)
;
US-10-409-701-8

```

Query Match	37.7%;	Score 373.8;	DB 13;	length 759;
Best Local Similarity	71.4%;	Pred. No. 1.7e-98;		
Matches 492; Conservative	0;	Mismatches 197;	Indels 0;	Gaps 0;

QY	215	CTTCCGTACTACGGGTGGCTGCGACAGACGGCCACGCCACCTTTTATGTGTGTGTAACG	274
Db	71	CCGGCGTCGACTACGGGCTCGTGGCAGAGCGGCCACGCCACGTTCTACGGCGCGCGCGACG	130
QY	275	CATCTGGCACCATGGGTGGAGCTTGTGGGTATGGGAATTTATACGCCCAAGGGTATGGCA	334
Db	131	CGTCTGGCACGATGGGGCGCGCTGCGGCTACGGGAACATGTACAGCACGGGGTACGGCA	190
QY	335	CGAACACGGGTGGCGCTGAGCACTGCGCTATTTAACAATGGATTAGTTGTGTGCTTGTCT	394
Db	191	CCAACACGGCGCGCTGAGCACGGCGCTGTTCACACGACGGCGCGCGGTGCGGTCTGTCT	250
QY	395	TCGAATGACTTGTACAAACGACCCTTAATGTGGCTTCCGGGAATAATTAGGTCAC TG	454
Db	251	ACGAGCTGCGCTGCGACAAACGGGCACTGTTGCTTCCGGGACCATCACCGG	310
QY	455	CCACCAACTTTTGGCCCTCTTAATTGTCTCTCCCTAACAAACAATGGTGGATGTGCAAC	514
Db	311	CCACCAACTTCTGCCCGCCCACTACGGGCTTCCAGCAGACGGCGGCTGTGCAAC	370
QY	515	CTCCTCTCCAACTTTCGACATGGCGTGAGCGCTGCTTCTTCAAAATCGCTCAATACGAG	574
Db	371	CGCGCGCGCCACTTCGACATGGCCAGCCGCGCTTCTCCAGATCGCGCAGTACCGCG	430
QY	575	CTGGTATCGTCCCGCTCTCCTTTCGTAGGGTACCATGTATGAAGAAAGGTGAGTGAAGT	634
Db	431	CCGGCATCGTGCCTCGCTTACAGAGAGGTGCTGCTGAAGAAGGGCGGATCAGT	490
QY	635	TTACAATCAATGGCCACTCATCTTCAACCTCGTTTGATCACAACGTCGGTGGCGAG	694
Db	491	TCACCATCAACGGCCACTCTTACTTCAACCTGTGTGTGACCAACGTGGCGGCGCG	550
QY	695	GCGAGCTCCACTCTGTGTGATAAAGGGGTTCGAACCTGGATGGCAATCCATGTCTAGAA	754
Db	551	GGGAGCTGACGTCCGTGTCCATCAAGGGCTCCAGCACCGGATGGCAAGCCCATGTCCGCA	610
QY	755	ATTGGGGCCAAACTGGCAAGCAACAACATATCTCAATGGCCAAAGGCTTCTTTCAAG	814
Db	611	ACTGGGGCCAGAACTGGCAGAGCAACTCGCTCTCGACGGCCAGAGCCTGTCTTCCAGG	670
QY	815	TCACTCTTAGTGATGTGCGCACTTCACCTGCTTAATATCTCGTTCCTTCCAAATGGCAAT	874
Db	671	TCACCGCCGACGACGGCGCGCATCGTCAACCAAGCAACGGCGTCCGCTCGGGCGGTGGCAGT	730
QY	875	TTGGCCAAACCTATGAAGGCCCTCAATTC	903
Db	731	TCGGCCAGACTTTCGAGGGCGGCCCAAGTTC	759

RESULT 5
US-09-938-842A-91

```

: Sequence 91, Application US/099338842A
: Patent No. US20020160378A1
:
: GENERAL INFORMATION:
: APPLICANT: Harper, Jeff
: APPLICANT: Krebs, Joel
: APPLICANT: Wang, Xun
: APPLICANT: Zhu, Tong
: TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
: TITLE OF INVENTION: SAME, AND METHODS OF USE
: FILE REFERENCE: SCRIP1300-3
: CURRENT APPLICATION NUMBER: US/09/938,842A

```


OY 902 TC 903
Db 740 TC 741

RESULT 7
US-09-938-842A-89

; Sequence 89, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 89
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-89

Query Match 34.4%; Score 341.6; DB 10; Length 774;

Best Local Similarity 69.9%; Pred. No. 4.3e-89;

Matches 477; Conservative 0; Mismatches 199; Indels 6; Gaps 1;

OY 228 CGGTGGCTGGCAGCGGCCACCCCTTTATGCTGTGTGACGCATCTGGCACCAT 287
Db 84 CGGCGCATGGCAAAACGACACCGCCACTTTTACGGTGGCAGCGACCGCTCCGGCAAT 143
OY 288 GGGTGGAGCTGTGGGTATGGAAATTATACAGCCCAAGGGTATGGCAGCAACGGTGGC 347
Db 144 GGGAGAGCTGTGTGTACGGTAACTATACAGCCCAAGGGTATGGCAGCAACGGTGGC 203
OY 348 GCTGAGCACTGGCTATTAAACAATGATTAAGTGTGTGCTTCTGAAATGACTTG 407
Db 204 TTGAGTACGGGCTGTTAAACAATGATTAAGTGTGTGAGCTTGTGAGCTTAAATG 263
OY 408 TACAACGACCTTAATGTGTCTCCGGGAA-----CTATTAGGGTCACTGCCACCA 461
Db 264 CGCCAACGACCTCAATGTGTCACTCAGGTAGTCTTCATCTCATCACCGCAACCA 323
OY 462 CTTTGGCCCTCTTAACCTTGTCTCCCTAACAACAATGTGTGATGTGCAACCTCTCT 521
Db 324 TTTCTGCCCAACCAACTTGGCTAGCTAGCGAACAAGAGATGTGCAACCCACG 383
OY 522 CCAACACTTGCATGAGCTGAGCTGCTCTTCAATCGTCAATACCGAGCTGTAT 581
Db 384 TGAACACTTGCATGAGCTGAGCTGCTCTTCAATCGTCAATATCGCGCGCAT 443
OY 582 GTCCCGCTCTCTTCTGAGGATCACTGATGAAGAAAGTGAAGTGAAGTTTAAAT 641
Db 444 TGTCCCGCTCTATACCGCAGGCTGCAATGTAAGAAAGAGAGGAGCATTAAGTTCA 503
OY 642 CAATGGCACTGATCTTCAACCTCGTTTGAATCAAAACGTGGTGGCGAGCGAGCT 701
Db 504 CAACGCTACCGTTACTTCAACTGGTCTGATCACTAACGTGGCTGGAGCAGAGACAT 563
OY 702 CCACTGTGTGTGAATGAAGGGGTCTGAAGTGAAGCAATCATGTCTAGAAATGGGG 761
Db 564 GTGAGGGCTAGTGTGAAGAGATCAAGGAGTGTGATGATTTGAGCAGAAACTGGGG 623
OY 762 CCAAACTGGCAAAAGCAACATATCTCAATGGCCAAAGGCTTCTTCAAGTCACTCT 821

Db 624 ACAAACTGGCAATCTAATGCTGTTTGGTGTCAAGCACTCTTTCGGTGCACAGG 683
OY 822 TAGTATGCTGCACACTCTACTGCTATATCTGTTCTTCCAAATGGCAATTTGGCCA 881
Db 684 CAGTACCGTGAACATCTACTTCTGGAACATGTTCTTCTTAAGTGGCAGTTTGTCA 743
OY 882 AACCTATGAAGCCCTCAATTC 903
Db 744 AACCTTGTGCGGAAGAATTTTC 765

RESULT 8

US-09-938-842A-842

; Sequence 842, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 842
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-842

Query Match 30.4%; Score 301.2; DB 10; Length 774;

Best Local Similarity 67.0%; Pred. No. 2.8e-77;

Matches 445; Conservative 0; Mismatches 213; Indels 6; Gaps 1;

OY 229 GGTGGCTGGCAGCGGCCACCCCTTTATGCTGTGTGACGCATCTGGCACCATG 288
Db 85 GGTGGTGGGAAACTGCTACCGCCACTTTCTACGGTGGCTGTGATGCTTCTGGAACAATG 144
OY 289 GGTGAGCTTGTGGGTATGGGAATTATACAGCCCAAGGGTATGGCAGCAACGGTGGCG 348
Db 145 GGAGAGCTTGTGTATGTATGTAATTAATACAGCCCAAGGGTATGGTGAACAGCGGCGCT 204
OY 349 CTGAGCACTGCGCTATTAAACAATGATTAAGTGTGTGCTTCTGAAATGACTTGT 408
Db 205 TTAAGCAGCGCTCTGTTCAACAATGTTTATGCTGTGTGCTTCTTGAAGCTCAATGT 264
OY 409 ACAACGACCTTAATGTGTCTCCGGGAA-----CTATTAGGGTCACTGCCACCAAC 462
Db 265 GCTAGTATCAAAATGTGTCCATTCTGTGATGCTTCAATCTTCACTGCGACTAAT 324
OY 463 TTTGCTCTCTTCTTCTGATGCTCTCCCTAACAACAATGTGTGATGTGCAACCTCTCTC 522
Db 325 TTTGCTCTCTTCTTCTGATGCTCTCCCTAACAACAATGTGTGATGTGCAACCTCTCTA 384
OY 523 CAACACTTGCATGAGCTGAGCTGCTCTTCAATCGTCAATACCGAGCTGTATC 582
Db 385 CCTCACTTGTATCTTGTATGCTCTATGTTCTCAAGATCGTGAATCGTCCGGAATC 444
OY 583 GTCCCGCTCTCTTCTGATGGGTATCAATGATGAAGAAAGTGAAGTGAAGTTTCAATC 642
Db 445 GTCCCGCTCTCTTCTGATGGGTATCAATGATGAAGAAAGTGAAGTGAAGTTTCAATC 504
OY 643 AATGGCACTCATCTTCAACCTGTTTGAATCAAAACGTGGTGGCGGAGGAGCTC 702

Db	505	AACGCGTTTCCGTTATTTTAACTTGGTTC TAGTCAC TTAACGCTGCGCGCCGGAACATA	564
Qy	703	CAC TCTGTGTCGATAAAGGGGCTCTCGAACTGGATGGCAATCCATGTCTTAGAAATTGGGGC	762
Db	565	GTGCGCGCTAGGTGTGAAAGGAACACATATCTTCGTGATGACCATGAGTCGTAAC TGGGGA	624
Qy	763	CAAAACTGGCCAAAGCAA CAACTATCTCAA TGGCCAAAGGCGCTTTCCTTCAAGTCACTCTT	822
Db	625	CAAAACTGGCAATCTAACTCACTGTTTGGTTGGTCA GTCACATTTCTTTAGAGTCA CAAGC	684
Qy	823	AGTGTAGGTGCGCACTCTCACTGCCTATAA TCTCGTTCCTTCCAATTGGCAATTGGCCAA	882
Db	685	AGTGAACCGTAGAAGCTCGACGTCGTGGAACAT TGTCTCCGGCGAATTGGAAGTTGGTCA G	744
Qy	883	ACCT 886	
Db	745	ACTT 748	

RESULT 9

```

US-09-770-445-491/C
; Sequence 491, Application US/09770445
; Patent No. US20020023281A1
;
GENERAL INFORMATION:
;
APPLICANT: Gorlach, Jörn
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Matchew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Woessner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Kriker, Maja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Huthan, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2023US (PARA-012PRV)
CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 491
;
LENGTH: 893
;
TYPE: DNA
;
ORGANISM: Arabidopsis thaliana
;
FEATURE:
;
NAME/KEY: misc_feature
;
LOCATION: (1) ... (893)
;
OTHER INFORMATION: n = A,T,C or G
;
US-09-770-445-491

```

Query Match	30.1%;	Score 298.8;	DB 9;	Length 893;
Best Local Similarity	66.6%;	Pred. No. 1.5e-76;		
Matches 442; Conservative	0;	Mismatches 216;	Indels 6;	Gaps 1

[illegible]

QY	349	CTGAGCAGCTGCCTATTAAACAATGATTAACTTGCTGCTTGCCTTCCAAATGACTTGT	408
Db	654	TTAAGCAGCGCTCTGTTCAACAATGGTTTAGCTGTGGTCTTGTTTTGAAGCTCAATGT	595
QY	409	ACAAACGACCCTAAATGCTGCCCTCCGGAA-----CTATTAGGGTCACTGCCACCAAC	462
Db	594	GCTAGTGATCCAAATGGTGCCATTTCTGTAGTCTTCAATCTTCAATCACTGCCACTAAT	535
QY	463	TTTTGCCCTCCTAATTGCTCTCCCTAACCAACAATGGTGATGGTGCAACCTCTCTTC	522
Db	534	TTCTGTCTCCGAACCTTGTCTCAGCCTAGTACAAATGGTGGTGGTAAACCTCCTAGA	475
QY	523	CAACACTTGACATGGCTGAGCCTCCTTCTTCAAATCGCTCAATACCGAGCTGTATC	582
Db	474	CCTCACTTTGATCTTGCTATGCTATGTTTCTCAAGATCGCTGATATCGTGCCGAATC	415
QY	583	GTCCCGCTCTCTTTCGTAGGGTACCATGTATGAAGAAAGGTGAGTGAGTTACAATC	642
Db	414	GTCCCGCTCTCTTCCCGCAGTGCCATGCCGAAGAGAGAGAAATTAAGTTACAATC	355
QY	643	AATGGCCACTCATCTTCAACCTCGTTTGTATCAGAAACGTCCGTGGCCAGGCACTC	702
Db	354	AACGGTTCCGTTATTTAACTTGGTTCTAGTCACTAAAGTNNNNNGCCCGGAAACATA	295
QY	703	CACCTCTGTGCGATAAAGGGGTCTGCAACTGATGGCAATCCATGTCTAGAATTTGGGC	762
Db	294	GTGGCGCTAGGTGTGAAGAAAGAACACATACTTCGTGGAATGACCATGATCGTAACCTGGGA	235
QY	763	CAAAACTGGCAAGCAACAATATCTCAATGGCCAAAGCCTTTCCTTCAAGTCACTCTT	822
Db	234	CAAAACTGGCAATCTAACTCAGTTTGGTTGGTCACTCACTTCTTTTGAAGTCAACAAGC	175
QY	823	AGTATGCTGCGCACTCTCACTGCTATAATCTCGTTCTTCCAATTGGCAATTTGGCCAA	882
Db	174	AGTACCGGTAGAAGCTCGACGCTGTGGAACATTCCTCCGGCAATTGGAAGTTGGTCAAG	115
QY	883	ACCT 886	
Db	114	ACTT 111	

RESULT 10

```

US-09-878-574-3973
; Sequence 3973, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878, 574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333, 535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3973
; LENGTH: 410
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-003-Q1-B1-D9
US-09-878-574-3973

```

Query Match	27.2%;	Score 270;	DB 10;	Length 410;
Best Local Similarity	79.1%;	Pred. No. 2.5e-68;		
Matches 321; Conservative	0;	Mismatches 85;	Indels 0;	Gaps 0;

QY 488 CTAAACAATGGTGATGGTGCAACCTCTCTCAACAATTGCATGGCTGAGCCTG 547
|||||
Db 3 CTAAACAATGGTGCTGGTGCAACCTCTTGCACAACCTTGATCTTGGCTGAGCCTG 62

QY	548	CCCTTCCTTCAAAATCGCTCAATACCGAGCTGGTATCGTCCCGCTCTTTCGTAGGGTAC	607
Db	63	CTTTCCTTGCAAAATGCTCAATACAAAGCTGGAATTGTTCCAGTTTCTTCAGAAAGAGTCT	122
QY	608	CATGTATGAAGAAAGGTGGAGTGAGGTTTACAATCAATGGCCACTCATACTTCAACCTCG	667
Db	123	CTGTGTGAAGAAAGAGGGATCAGGTTCAACCATCAATGGTCACTCTTAATTCAACTTGG	182
QY	668	TTTTGATCACAAAGCTCGGTGGCGCAGCGACGTCACTCTGTGCAATAAGGGGTTC	727
Db	183	TTCATCATCAAAATGTGTGGTGAGCTGGAGATGTTCAATTCTGTCCATCAAAAGGCTCA	242
QY	728	GAACTGGATGGCAATCCATGTCTAGAAATTGGGGCCAAACTGGCAAGCACACACTATC	787
Db	243	GAACTGGGTGGCAAAACCATGTCTAGAACTGGGGGCAGAAATTGGTAAAGCAACTCTTACC	302
QY	788	TCAATGGCCAAAGGCTTTCTTCTTCAAGTCACTCTTAGTGATGGTGGCACTCTCACTGCT	847
Db	303	TGAATGGCCAAAGCTCTCTTTTTCAGGTCACTACAAGTGATGGCAGGACTCTCACTAGCA	362
QY	848	ATAATCTCGTTCCTTCCCAATTGGCAATTTGGCCAAACCTATGAAG	893
Db	363	ACAACATTTGTGCTGTGCTAACTGGCAATTTGGACAAACATTTGAAG	408

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RESULT 11
US-09-938-842A-1046
; Sequence 1046, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1046
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1046

```

Query Match	25.3%;	Score 251.2;	DB 10;	Length 768;
Best Local Similarity	61.9%;	Pred. No. 1.1e-62;		
Matches 454; Conservative	0;	Mismatches 268;	Indels 12;	Gaps 3;

[illegible]

Db	252	GTGATGCAACCAAGTACCA	CAATGCTGTCTTAAGCAATCA	CTACTATCACAGC	311							
QY	456	CACCAACTTTG	CCCTCCTA	CTTGTCTCCCTA	CAACATG	TGTGATG	TGCAACC	515				
Db	312	TACAAACTTCTG	TCCACCGA	CTTGTCTCAGGCA	AGCAATG	AGGTG	TGCAACC	371				
QY	516	TCCTCTCCA	CACCTTGC	ACATG	GTGAGCCTG	CTTCTCA	ATCGCTCA	TACCGAGC	575			
Db	372	ACCGAGACCT	CATTTCG	ACATGGCTC	AGCCTG	CGTTTCTC	ACCATTG	CTAAGTACA	AGC	431		
QY	576	TGCTATCGT	CCCCGTC	CTCTTTCG	TAGGGTAC	CATGTATGA	AGAAAG	TGAGTGA	GT	635		
Db	432	TGGAATCGT	CCCCCAT	TTCTTACA	AAAAAGT	TGATGTAG	AAGACCG	AGGATG	AGATT	491		
QY	636	TACAATCA	TATGGCCACT	CATCTCA	CTCGTTTGA	TACAAAC	GTGCGTGG	CGCAGG	695			
Db	492	TACAATTA	ACGGTAGA	AACTATTTC	AGCTTGTTC	TCACTCAA	ACGTA	GCAGAGG	GGG	551		
QY	696	CGAGCTCC	ACTCTGTG	TGATTA	AGGGGTCT--	CGAACTG	ATGGCA	TCCATGT	CTAG	752		
Db	552	TGAGATCT	CTTAAGTT	TGGATCA	AAAGATCTA	AGGCAACA	AAATGGG	AGACA	TGTCAAG	611		
QY	753	AAATTGGG	GGCCAAA	CTGGCA	AGCA	CACTATCTCA	ATGGCC	AGGCTTT	CTTTCA	812		
Db	612	AAATTGGG	AGGAGCTA	ATTATC	AGAGTA	TACTTAC	CTTAATG	GTCAATCT	TATCTTTCA	671		
QY	813	AGTCACT	CTTAGT	ATGTTG	CTGC	ACTCTCA	CTGCTTA	TATCTG	TTCTTCCA	ATTGGCA	872	
Db	672	AGTTCA	ACTTAG	TATG	GAATGA	AGTAATCA	AGCAGCT	CTCA	CGTTG	TCTTGA	ATTGGCG	731
QY	873	ATTGGC	CAAACT	886								
Db	732	GTTTGGT	CAGAGCT	745								

```

RESULT 12
US-09-878-574-62
; Sequence 62, Application US/09878574
; Patent No. US20020110548A1
GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 62
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(391)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3028-056-Q1-B1-E10
US-09-878-574-62

```

Query Match	25.3%	Score 251;	DB 10;	Length 391;
Best Local Similarity	77.8%;	Pred. No. 8.6e-63;		
Matches 302; Conservative	0;	Mismatches 86;	Indels 0;	Gaps 0;

OY	499	GGTGGATGGTGCACACCCTCTCTCCACACACTTCCACATGGCTGAGCTGCCCTTCTTCAA	558
Db	1	GGTGGTGGTGCACACCCTCTCTGCACACACTTGTATATGGCTGAACCTGCTTCTTCAA	60
OY	559	ATGCTCAATACCGAGCTGTATCTGCCCGTCTCTTTCGTAGGGTACCATGTATAGAG	618

Db	61	ATTGCTGAATATATAGAGCTGGAAATTGTCCTGTGGCCTTTCAGGAGGGTTCCTGTGTGAAA	120
Qy	619	AAAGGTGAGTGAAGTTTACAATCAATGAGCCACTCATATCTCAACCTCGTTTGATCA	678
Db	121	AAGGAGGAATTAAGTTTACAATCAATGAGCCACTTTCCTCAACCTTAAGTTTGATCAC	180
Qy	679	AACGTGCGTGGCGCAGGCGGACGTCCACTCTGTGTGATTAAGGGGTCTGGAACGTGATGG	738
Db	181	AATGTGGCTGGAGCTGCTGTGATGTGAATTCAGTGTCCATTAAAGGGTCCAAAACTGGGTGG	240
Qy	739	CAATCCATGTCTAGAAATTGGGGCCAAAACTGGCAAAAGCAACAATATCTCAATGGCCAA	798
Db	241	CAGCCCATGTCAAGAAACTGGGGGCCAAAACTGGCAGAGCAACTCATACTCAATGACAA	300
Qy	799	GGCCTTTCCTTCAAGTCACTCTTAGTGAATGTGTGCACCTCTCACTGCCTAATCTCGTT	858
Db	301	TCNCTCTCTTTTCAAGTCAACCACCATGATGAGCAGAACTGTGACAAGCTTCAATGTGCA	360
Qy	859	CCTTCCAATTGGCAATTTGGCCAAACCT	886
Db	361	CCAGCCAAATTGGCAATTTGGCCAGACCT	388

RESULT 13

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US-09-770-791-430
; Sequence 430, Application US/09770791
; Patent No. US20020062014A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kriker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2029 (PARA-018PRV)
; CURRENT APPLICATION NUMBER: US/09/770,791
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,480
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 430
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-791-430

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Query Match	17.1%;	Score 169.2;	DB 9;	Length 366;
Best Local Similarity	71.7%;	Pred. No. 6.6e-39;		
Matches 238; Conservative	0;	Mismatches 88;	Indels 6;	Gaps 1;

[illegible]

OY		348	GCTGAGCACC	TGCCTATT	TAACAATGGA	TTAAGTGTGGTGCTTCGAAATGACTTG	407
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OY		408	TACAAACGAC	CCCTAAAT	GTGTGCC	TTCCGGGAA-----CTATTAGGGTCACTGCCACCAA	461
Db		215	TACTGATGAT	CCGAGATG	TGTGTTC	CCGGAAATCCATCTATTCTTGACCGCGCACAA	274
OY		462	CTTTTGGCC	CTCCTAAC	TTTGCTCT	CCCTAACACAATGTTGATGTTGCAACCCCTCCTT	521
Db		275	CTTTTGTCCG	CCGAATTT	TGTCTCAG	CCGAGTAGCAGACGGAGGTGTGCAATCCGCCGC	334
OY		522	CCAACACTT	CGACATGG	CTGAGCCTG	CCTTCC	553
Db		335	CGAGCATTT	TGATCTCG	CCCATG	CCCTATGTTCC	366

RESULT 14

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US-09-878-574-3468
; Sequence 3468, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3468
; LENGTH: 373
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-010-Q1-B1-E9
US-09-878-574-3468

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Query Match	15.0%;	Score 149;	DB 10;	Length 373;
Best Local Similarity	74.3%;	Pred. No. 5.3e-33;		
Matches 188; Conservative	0;	Mismatches 65;	Indels 0;	Gaps 0;

QY	222	TGACTACGGTGGCTGGCAGAGCGGCCACGCCACCCTTTATGTGTGTGTGCATCTGG	281
Db	65	TGTGTTTTGGAGTTGGACCAATGCATGCCACCTTCATGAGGGGGTGATGCTTCTGG	124
QY	282	CACCATGGGTGAGCTTGTGGTATGGGAATTATACAGCCAAAGGTAATGGCAGAACAC	341
Db	125	GACAATGGGTGGGGCTGTGTGTTATGGAATCTGTATAGCCAAGGTTATGGAATGATAC	184
QY	342	GGTGGCGCTGAGCACTGCGCTATTTAACAATGATTAAGTTGTGTGCTTGCTTGAAT	401
Db	185	AACAGCACTGAGCACTGCACCTGTTCACAACATGGCTTAAGCTGTGTGCATGCTTCAAT	244
QY	402	GACTGTACAACGACCCTAATATGTGCTTCCGGAACTATTAGGTCACCTGCCACCA	461
Db	245	TAAATGTGCGAATGACCCACAATGTGCTTCTCGGCTCCATCATAGTCACTGCCACAA	304
QY	462	CTTTTGCCCTCCT	474
Db	305	TTTCTGTCCACCT	317

RESULT 15

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US-09-878-574-1206
; Sequence 1206, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: la Rosa, Thomas J.

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 18, 2003, 20:41:56 ; Search time 2062 Seconds
(without alignments)
11692.551 Million cell updates/sec

Title: US-09-383-579C-9

Perfect score: 992
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
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6: em_estpl: *
7: em_estro: *
8: em_hic: *
9: gb_est1: *
10: gb_est2: *
11: gb_hic: *
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23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rod: *
26: em_gss_phg: *
27: em_gss_vr1: *
28: gb_gss1: *
29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	435.4	43.9	880	14	CD574577	CD574577 UCRPT01_0
2	435.2	43.9	798	10	BG581975	BG581975 EST483712
3	429.4	43.3	816	14	CD575807	CD575807 UCRPT01_0
4	422.2	42.6	809	14	CB291406	CB291406 UCRCS01_0

5	418.8	42.2	799	14	CB293003	CB293003 UCRCS01_0
6	418.6	42.2	838	14	CB980842	CB980842 CB970003
7	414.2	41.8	767	12	BI932999	BI932999 EST552888
8	411.4	41.5	681	14	CD484188	CD484188 atr01-4ms
9	410	41.3	786	13	BQ165503	BQ165503 EST611372
10	406	40.9	719	14	CA785153	CA785153 sau25c03.
11	404.8	40.8	864	14	CB822230	CB822230 EST 3081
12	404.6	40.8	878	14	CD574625	CD574625 UCRPT01_0
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14	402.6	40.6	815	10	BE131139	BE131139 L48-1090T
15	401.8	40.5	736	14	CD486517	CD486517 CRH3.3F02
16	400.8	40.4	788	14	CB290960	CB290960 UCRCS01_0
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20	394	39.7	859	14	CD574696	CD574696 UCRPT01_0
21	391.8	39.5	843	14	CB979649	CB979649 CAB70001
22	390.2	39.3	656	13	BQ986992	BQ986992 QGF10P22.
23	390.2	39.3	868	10	BG446553	BG446553 GA_Eb003
24	386.6	39.0	966	10	BE055631	BE055631 GA_Eb003
25	380.4	38.3	620	13	BU044752	BU044752 PP_LEa002
26	378.8	38.2	688	14	CB007302	CB007302 VVCO43G12
27	377.6	38.1	611	13	BU044997	BU044997 PP_LEa002
28	377	38.0	1106	11	AY104146	AY104146 Zea mays
29	375	37.8	741	12	BI309709	BI309709 EST531119
30	374.4	37.7	730	14	CA917809	CA917809 EST641956
31	374	37.7	685	13	BU815493	BU815493 N042D11.P
32	373.8	37.7	617	13	BQ852261	BQ852261 QGB17122.
33	373.6	37.7	580	13	BU763038	BU763038 sa836e03.
34	373.2	37.6	723	14	CB292105	CB292105 UCRCS01_0
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36	371.4	37.4	706	10	BF479593	BF479593 L48-3281T
37	370.6	37.4	699	14	CA840495	CA840495 MCT038A10
38	369.8	37.3	757	13	BU007051	BU007051 QGH13D18.
39	367.2	37.0	656	13	BU892415	BU892415 P063C07.P
40	367.2	37.0	710	12	BI931078	BI931078 EST550967
41	366.6	37.0	656	13	BU893884	BU893884 P084A04.P
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ALIGNMENTS

RESULT 1
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LOCUS UCRPT01_06_G11_T3 Poncirus trifoliata CTV-challenged cDNA library -
DEFINITION UCR Poncirus trifoliata cDNA clone UCRPT01_06_G11, mRNA sequence.
ACCESSION CD574577
VERSION CD574577.1 GI:31670479
KEYWORDS EST.
SOURCE Poncirus trifoliata
ORGANISM Poncirus trifoliata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Sapindales; Rutaceae; Poncirus.
REFERENCE 1 (bases 1 to 880)
AUTHORS Roose,M.L., Ye,X., Federici,C.F., Close,T.J., Fenton,R.D.,
Wanamaker,S., Choi,Y. and Kingan,T.
TITLE Development of EST Resources and New Genetic Markers for California
Citrus - Poncirus trifoliata CTV-challenged phloem - UCR
JOURNAL Unpublished
COMMENT Contact: Mikeal Roose
Department of Botany & Plant Sciences, University of California
Riverside, CA, 92521-0124, USA
Tel: 9097874137
Fax: 9097874437
Email: mikeal.roose@ucr.edu
Seq primer: T3.
FEATURES Location/Qualifiers

Db	226	TGGGTATGGCAATTGTATACAGCCAAAGCTATGGACTAATACACTGACGACCTTAGTACC	285
Oy	360	GCTATTTAAACAATGATTAAGTTGTGGTCTTGCTTCGAAATGACTTGTACAAACGACCC	419
Db	286	TCTATTCAACAATGGCCTTAAGCTGTGGTTTCATGTCTATGAAATGAAATGTGAAAAATGACCC	345
Oy	420	TAAATGGTGCCCTTCCGGGAACTATTAGGGTCACTGCGCAACCACTTTGCCCCCTTAACCTT	479
Db	346	CAAGTGGTGCTCCCGGCTCCATCATTTGTACCGGCACCAACTTCTGCCCCACTTAACCT	405
Oy	480	TGCTCTCCCTAACAAACAATGTTGATGTTGTCMAACCTCTCTCCAAACTTTCGACATGGC	539
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Oy	540	TGAGCTGCGCTTCCCTTCAAAATGCTCATATACCGAGCTGTATGTCGCCGTCCTTTCG	599
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RESULT 4
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 LOCUS
 DEFINITION
 CB291406 809 bp mRNA linear EST 28-FEB-2003
 UCRCS01_02dd11 g1 Washington Navel orange cold acclimated flavedo &
 albedo cDNA library Citrus sinensis cDNA clone UCRCS01_02dd11, mRNA
 sequence.
 CB291406
 CB291406.1 GI:28616863
 EST.
 Citrus sinensis
 Citrus sinensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Sapindales; Rutaceae; Citrus.
 1 (bases 1 to 809)
 Close, T.J., Collura, K., Fenton, R.D., Feuerbacher, O., Kim, H.R.,
 Kudrna, D., Wanmaker, S., Wing, R. and Yu, Y.
 Development of EST Resources and New Genetic Markers for California
 Citrus
 Unpublished
 Contact: Timothy Close
 Department of Botany & Plant Sciences, University of California
 Riverside, CA, 92521-0124
 Tel: 9097873318
 Fax: 9097874437
 Email: timothy.close@ucr.edu
 Seq primer: T3.
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 source
 location/Qualifiers
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 /mol_type="mRNA"
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		/tissue_type="Rind containing flavedo and albedo"
		/dev_stage="Mature fruit"
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		/note="Vector: lambda Uni-ZAP XR, excised phagemid; site_1: EcoRI, site_2: XhoI; Plants were grown in the field at University of California, Riverside Agricultural Operations since 1983. The scion was Washington Navel orange and the rootstock Carizzo Citrange. Tissue from mature fruit was harvested at mid-day in January 2002 during a cold spell, when pre-dawn temperatures were approximately -2 to 2 degree C. Approximately 2 cm median sections of the rind were excised in the field from several fruits, then wrapped in aluminum foil and frozen quickly in dry ice. Total RNA was extracted using a pheno- extraction procedure described in J. Japanese Soc. Hort. Sci. (1996) 64:809-814. Poly(A) RNA was purified, a cDNA library was made, and 1 million primary lambda cDNA clones were in vivo excised to give a population of Bluescript SK(-) phagemids. All steps to this point were performed in the TU Close lab at the University of California, Riverside (Fenton). Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3530 at the Arizona Genomics Institute, University of Arizona (Collura , Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Wanamaker) using the Harvest pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."

BASE COUNT	210	a	196	c	191	g	212	t
ORIGIN								

Query Match	42.6%	Score	422.2;	DB	14;	Length	809;		
Best Local Similarity	75.8%;	Pred.	No. 1.5e-56;						
Matches	536;	Conservative	0;	Mismatches	168;	Indels	3;	Gaps	1

QY	183	TCTCTTTCTTCTTCCTTCTTCTTCTTGTGCTTACCTTGCGTGAATA--CGGTGGCTGGCA	239
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QY	240	GAGCGGCCACGACCCTTTATGTGTGTGTGACCATCTGGCACATGGGTGAGCCTTG	299
Db	162	AAGTGGCCATGCACTTCTATGGCGGGGTGATGCTTCCGGCAATGGGTGTCTTG	221
QY	300	TGGTATGGGAATTATATACAGCCAAAGGTATGGCAGAACACGGTGGCGGTGAGCACTGC	359
Db	222	TGGTATGGCAATTTGTACAGCCAAAGCTATGGACTTAACACTGCATCACTCAGTACCGC	281
QY	360	GCTATTTAACAATGGAATTAAAGTTGTGTGCTTGCTTGGAAATGACTTGTACAAACGACCC	419
Db	282	TCTATTCAACAATGGCCTAAGCTGTGTGCTCATGCTAATGAATGAATGTGAAAATGACCC	341
QY	420	TAAATGTGCTTCGCGGAACTATTAGGGTCACTGCCCCAACCACTTTTGCCCTCTTAATT	479
Db	342	CAGTGTGCTCCCGGCTCCATCATTTGTACCGGCCAACCACTTCTGCCACCTTAACCT	401
QY	480	TGCTCTCCCTTAACAACAATGTGTGATGTGCAACCTCTCTTCCAACAACCTTGACATGGC	539
Db	402	TGCTCTGTCTAAGCACAACGCGGTGTGTCAATCTCCCTCCAGCACTTTGACATGGC	461
QY	540	TGAGCTGCTTCCTTCAAAATCGCTCAATACCGAGCTGTATCGTCCCGCTCTCTTTG	599
Db	462	TGAGCCCGCTTTCTTGCAAATTTGCCAATACCGCGCGGTATCGTCCCAATTTCTTCAG	521
QY	600	TAGGTCACCATGTATGAAGAAGGTGAGTGAGGTTTCAATCAATGGCCACTCATACTT	659
Db	522	AAGATCCCGTGTGCGAAGAAAGAGAAATTAAGGTTTACCGTCAATGACACTCATACTT	581
QY	660	CAACTCGTTTTGATCACMAACGTCGTGGCGGAGCGAGCTCACTGTGTGATNAA	719

Db	Accession	Source	Organism	Reference	Authors	Title	Journal	Comment	Features
Db	582	CAACTGTTTTCATCACAAATGTCGAGAGCAGAGATGTACATTCAATCAATCAA	641						
Db	720	GGGGTCTCGAAGCTGATGGCAATTCATGTCAGAAATTTGGGCCAAATGGCAAGCAA	779						
Db	642	GGGTTCAAGAGCTGATGGCAAGCAATGTCAAGAACTGGGGCCAAATTTGGCAAGCAA	701						
Db	780	CAACTATCTCAATGGCCAAAGCCTTTCTCTTCAATGGCAATTTGGCCAAACCT	839						
Db	702	TTCTTATCTTAAACGGGCAAAAGCTTTCTTCTTCAATTTGACAGCCAGTGACGGCAGACTGT	761						
Db	840	CACTGCTTAAATCTCTGTTCTTCTTCAATTTGGCAATTTGGCCAAACCT	886						
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RESULT 5	CB293003								
LOCUS	CB293003								
DEFINITION	CB293003	799 bp	mRNA	linear	EST 28-FEB-2003				
ACCESSION	CB293003								
VERSION	CB293003.1	GI:28618460							
KEYWORDS	EST.								
SOURCE	Citrus sinensis								
ORGANISM	Citrus sinensis								
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids								
AUTHORS	1 (bases 1 to 799)								
TITLE	Close, T.J., Collura, K., Fenton, R.D., Feuerbacher, O., Kim, H.R., Kudrna, D., Manamaker, S., Wing, R. and Yu, Y.								
JOURNAL	Development of EST Resources and New Genetic Markers for California Citrus								
COMMENT	Unpublished								
CONTACT	Timothy Close								
DEPARTMENT	Department of Botany & Plant Sciences, University of California								
ADDRESS	Riverside, CA, 92521-0124								
TEL	9097873318								
FAX	9097874437								
EMAIL	timothy.close@ucr.edu								
SEQ PRIMER	T3.								
FEATURES	Location/Qualifiers								
SOURCE	1..799								
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	/clone="UCRCS01_05bf07"								
	/tissue_type="Rind containing flavedo and albedo"								
	/dev_stage="Mature fruit"								
	/lab_host="E. coli TUC121"								
	/clone_lib="Washington Navel orange cold acclimated flavedo & albedo cDNA library"								
	/note="Vector: lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; plants were grown in the field at University of California, Riverside Agricultural Operations since 1983. The scion was Washington Navel orange and the rootstock Carizzo Citrange. Tissue from mature fruit was harvested at mid-day in January 2002 during a cold spell, when pre-dawn temperatures were approximately -2 to 2 degree C. Approximately 2 cm median sections of the rind were excised in the field from several fruits, then wrapped in aluminum foil and frozen quickly in dry ice. Total RNA was extracted using a phenol extraction procedure described in J. Japanese Soc. Hort. Sci. (1996) 64:809-814. Poly(A) RNA was purified, a cDNA library was made, and 1 million primary lambda cDNA clones were in vivo excised to give a population of phagemid SK(-) phagemids. All steps to this point were performed in the TJ Close lab at the University of California, Riverside (Fenton). Phagemids were plated, plasmid DNA								

purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3530 at the Arizona Genomics Institute, University of Arizona (Collura, Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Manamaker) using the HarVEST pipeline (<http://harvest.ucr.edu>) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."

BASE COUNT	208 a	195 c	189 g	207 e
ORIGIN				

Query Match	42.2%;	Score 418.8;	DB 14;	Length 799;
Best Local Similarity	75.8%;	Pred. No. 5.1e-56;		
Matches 532; Conservative	0;	Mismatches 167;	Indels 3;	Gaps 1;

QY	183	TCCTCTTCTCTCTCTTCTCTTCTTGTCTTCACTTCGCTGACTA--CGGTGGCTGGCA	239
Db	98	TTTGTCTGCTCAATTTTGTCTTTCGTGGCACAATTGGAGACTATGCTGTGGTGGCA	157
QY	240	GAGCGGCCACGCCCACTTTATATGCTGTGTGTGACGCATCTGGCACCATGGGTGGAGCTTG	299
Db	158	AAGTGGCCATGCAACTTCTATGGCGGGGGTGATGCTTCCGGCACAAATGGGTGTCTTG	217
QY	300	TGGGTATGGGAATTATATACAGCCAAAGGGTATGGCACGAAACAGGTGGCGCTGAGCACTGC	359
Db	218	TGGGTATGGCAATTGTACAGCCAAAGCTATGGGACTAACACTGCAGCACTCAGTAACGC	277
QY	360	GCTATTTAACATGAGATTAAAGTTGTGTGCTTGTCTTGGAAATGACTTGTACAAAGACCC	419
Db	278	TCTATTCACAATGCGCTTAAGCTGTGTTGATGCTATGAAATGAAATGTGAAATGACCC	337
QY	420	TAAATGTGCTCTCCGGGAACTATTAGGCTCACTGCCACCACTTTTGCCCTCTAATT	479
Db	338	CAAGTGTGCTCTCCCGCTTCATCATTTGTCAACGCCACCAACTTCTGCCACCTAACC	397
QY	480	TGCTCTCCCTAACACAATGTGTGATGTGTGCAACCTCTCTCCAACACTTGACATGGC	539
Db	398	TGCCCTGTCTAACGACAAACGCGGTTGTGTGCAATCCTCCCTCCAGCACTTGACATGGC	457
QY	540	TGAGCCTGCTCTCTTCAATTCGCTCAATACCGAGCTGTATGTCGCCCGTCTCTTTCG	599
Db	458	TGAGCCCGCTTCTTGCAAATTGCCCAATACCGCGCGGTATGCTCCCAATTTCTTTCAG	517
QY	600	TAGGTACCATGTATGAAGAAGGTGAGTGAGGTTTACAATCAATGGCACCTACTT	659
Db	518	AAGGATCCCGTGTGCAAGAAGAAGAGAAATTAAGTTTACCGTCAATGACACTACTT	577
QY	660	CAACCTCGTTTTGATCACAAACGTGCGTGGCGCAGGCGACTCCACTCTGTCTCGATAA	719
Db	578	CAACCTGCTTTTGATCACAAATGTCGAGAGCAGAGAGATGTACATTCAATTCATCAA	637
QY	720	GGGCTCTCGAACTGATGCGCAATCCATGTCTAGAATTTGGGGCCAAAATTGGCAAAGCAA	779
Db	638	GGGTTCAAGACTGATGCGCAAGCAATGTCAAGAACTGGGGCCAAAATTGGCAAAGCAA	697
QY	780	CAACTATCTCAATGCGCAAGCGCTTCTCTTCAAGTCACTCTTAGTGATGCTCGCACTCT	839
Db	698	TTCTTATCTTAAACGCGCAAGCTTCTTCTTCCAAATTGACAGCCAGTGACGCGCAGGACTGT	757
QY	840	CACCTGCTATAATCTCGTTCCTTCCAAATGGCAATTTGGCCA	881
Db	758	GACTAGCAACAATGTTGTGCTTGAAATTTGGCAATTTGGGCA	799

RESULT 6	CB980842	838 bp	mRNA	linear	EST 01-MAY-2003
LOCUS	CB980842				
DEFINITION	Vitis vinifera CDNA clone CAB70003_1Iar_A03 3', mRNA sequence.				
ACCESSION	CB980842				
VERSION	CB980842.1	GI:30304048			

KEYWORDS	EST.
SOURCE	Vitis vinifera
ORGANISM	Vitis vinifera Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; Vitaceae; Vitis. 1 (bases 1 to 838) Goes da Silva,F., Iandolo,A., Lim,H., Baek,J., Jones,K. and Cook ,D.
TITLE	Expressed sequence tags from cabernet sauvignon berries at various developmental stages
JOURNAL	Unpublished
COMMENT	Contact: Douglas Cook, PhD CAES Genome Facility UC Davis, Plant Pathology One Shields Ave, Davis, CA 95616, USA Tel: 530 754 6561 Fax: 530 754 6617 Email: drccook@ucdavis.edu Seq primer: GCCAACGAATGGCTCTAG. Location/Qualifiers
FEATURES	1..838 /organism="Vitis vinifera" /mol_type="mRNA" /cultivar="Cabernet Sauvignon" /db_xref="taxon:29760" /clone="CAB70003.IIAR_A03" /sex="Hermaphrodite" /dev_stage="Post-Veraison, 18-19 brix" /lab_host="DH5alpha" /clone_lib="Cabernet Sauvignon Berry Post-Veraison - CAB7" /note="Organ: Berry; Vector: pDNR; Site 1: Sfil; Site 2: Sfil; CAB7 is a cDNA library of Cabernet Sauvignon Clone 8 berries. Samples were collected post-veraison from field-grown vines during stage III of berry growth at 89 days after full bloom. Berries soluble solid concentration ranged between 18-19 brix. Sampled vines were located at the University of California, Davis, Experimental vineyard. cDNAs were made by oligo-dT priming and directl onally cloned. 5'and 3' adaptors were used in cloning as follows: 5'-AAGCAGTGATTAACAACGACAGATGCCATTACGGCCGG-3' and 5'-ATTCTAGAGCGCCGAGCGGCAGCATG-dT(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."
BASE COUNT	192 a 233 c 219 g 194 t
ORIGIN	
Query Match	42.2%; Score 418.6; DB 14; Length 838;
Best Local Similarity	70.5%; Pred. No. 5.3e-56;
Matches	559; Conservative 0; Mismatches 234; Indels 0; Gaps 0;
QY	146 CCATCTTAGGCTTTTCTTACTCACCCCTTCCTCTCTCTTCTCTTCTCTTCTCTCT
DB	38 CAAATGGCTACTGCAGCATTTTCTTATCTCTCTTGCCCTTCTCTCTCTGTATGCC
QY	206 TTGCTTACCTTGCCTGACTACGGGTGGCTGGCAGAGCGGACCACCTTTATGGTG
DB	98 TCCAAGGCACAATAATGGTACTATGGTGGGTGGAGAAGTGCGCATGCCCATTATGGCG
QY	266 GTGGTGAAGCATGTGGCACCACCATGGGTGGAGCTTGGGGTATGGGAATTTATACCCAAG
DB	158 GTGGTGAAGCATGTGGCACCACCATGGGTGGAGCTTGGGGTATGGGAATTTATACCCAAG
QY	326 GGTAATGGCAGCAACGCGTGGCGCTGAGCACTGGCTATTAAACATGATTAAGTTGTG
DB	218 GGTAATGGCAGCAACGCGTGGCGCTGAGCACTGGCTATTAAACATGATTAAGTTGTG
QY	386 GTGCTTGCTTGAATGACTTGTAACAAGCACCCTAATGATGCTTCCGGAACTATTA
DB	278 GGGCATGTTAAGATGAATGACAGATGACCCCAAATGATGCTTCCAGGAGCCTAA
QY	446 GGGTACTGACCAACTTTTGCCCTCTAATTTGCTCTCCCTAACCAACATGGTGGAT

Db	338	CCGTGACTGCCAACAACTTCTGGCCCTCCTTAACCTTGCGCTTTGCCAACAACCAAGCGCAT	397
QY	506	GGTGCACACCCTCCTCTCCAACACTTCGACATGGCTGAGCCTGCCTTCTTCAAATCGCTC	565
Db	398	GGTGAATCCCCCTTCAGCACTTCGATCTAGCTGAGCCTGCCTTCTTCAAGATTGCC	457
QY	566	AATACCGAGCTGTATCGTCCCCTCTCCTTTCTGAGGCTAACATGTATGAAGAAGTG	625
Db	458	AGTACCGAGCTGAATCGTACTGTGTCTTTCAGAGAAGTCCCCTGTGTGAAGAAGAG	517
QY	626	GAGTAGGTTTACATCAATGAGCCACTCACTTAACCTCGTTTGTATCACAAACGTG	685
Db	518	GGATCCGCTTACCATCAACGGCCACTCCTACTTCAACTGTGTGCTCATCAACAGCTG	577
QY	686	GTCGCCGACGGCAGCTCCACTCTGTGTGATAAGGGGTCTCGAAGTGGATGGCAATCCA	745
Db	578	CCGAGCGGGAGACGTCAAGGACAGTATCATATAAGGGGTCTAAGACCGGTGGACGCCA	637
QY	746	TGTCTAGAAATTGGGGCCAAAACCTGSCAAAGCAACACTATCTCAATGGCCAGCCTT	805
Db	638	TGTCAAGGAAGTGGGGCCAGAACTGGCAGAGCACTCATACCTCAACGGCCAGACCTCT	697
QY	806	CCTTCAAGTCACTCTTAGTATGGTGGCCTCTCAGCTCTCATCTATATCTGTTCTTCCA	865
Db	698	CATTCGAAGTCAACGACGATGGCCGACCATGACACAGCCTCAATGTGGCCTGTG	757
QY	866	ATTGGCAATTGGCCAAACCTATGAAGGCCCTCAATTCTTAAACCATATACCCACACTGC	925
Db	758	GCTGCAGTTTGGGCAACATATGAGGGGCTCAGTTCTTAATTCTCACTAGTGTGTGC	817
QY	926	TATGACTACTACT	938
Db	818	TATGACTATGACT	830
RESULT 7	B1932999	767 bp mRNA linear EST 18-OCT-2001	
LOCUS	EST552888	tomato flower, 8 mm to preanthesis buds Lycopersicon	
DEFINITION	esculentum cDNA clone CTC024J22 5' end, mRNA sequence.		
ACCESSION	B1932999		
VERSION	B1932999.1	GI:16247471	
KEYWORDS	EST.		
SOURCE	Lycopersicon esculentum (tomato)		
ORGANISM	Lycopersicon esculentum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.		
AUTHORS	van der Hoeven,R.S., Bezzerides,J.L., Karamycheva,S.A., Tsai,J., Uteback,T., Van Aken,S., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.		
TITLE	Generation of ESTs from tomato flower tissue, buds 8 mm - preanthesis		
JOURNAL	Unpublished		
COMMENT	Contact: CUGI Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html This clone is available through the Clemson University Genomics Institute Seq primer: T3. Location/Qualifiers 1..767 /organism="Lycopersicon esculentum" /mol_type="mRNA" /cultivar="TA496" /db_xref="taxon:4081" /clone="CTOC24J22" /tissue_type="flower" /dev_stage="buds 8mm to preanthesis" /clone_lib="tomato flower, 8 mm to preanthesis buds"		
FEATURES	source		

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Cornell University; sequencing: The Institute for Genomic Research; flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."

BASE COUNT 215 a 144 c 168 g 240 t

Query Match 41.8%; Score 414.2; DB 12; Length 767;
Best Local Similarity 74.1%; Pred. No. 2.7e-55;
Matches 524; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

QY 199 TTCTTCTTGTCTTCACTTCCTGCTGACTAGCGTGGCGAGAGCGGCCACGCACTTT 258
DB 5 TTTTGCCTTCTATCTACTTTTGTGATTAAGAGATGGCAAACTGCTCATGCACTTTC 64
QY 259 TATGGTGGTGAGCGCATCTGGCAACCATGGGAGAGCTTGTGGTATGGAAATTATAC 318
DB 65 TATGAGAGGGGTATGCTCTGGCAATGGGGGTGCTTGTGATATGAAATTGTAT 124
QY 319 AGCCAAAGGATGACGACGAACACGGTGGCGCTGAGCACTGCGCTATTAAACAATGATTA 378
DB 125 AGCCAAAGGATGAACTAACAACAGTACAGCACTAGTACAGCACTATTCAACAATGTTTA 184
QY 379 AGTTGTGGTCTTGTCTTGAATGACTTTGCAAAAGACCTTAATGCTTCCGGA 438
DB 185 ACTTGTGGTCTTGTATGAGCTCACTTGAACAATGCACTCATGCTGTCTCAAGG 244
QY 439 ACTATTAGGCTGCTGACCAACCACTTTTGCCTTACTTGTCTTCCCTAACAAT 498
DB 245 ACTATTACTGCTGCACTAATAATTTTGTCTCCGAACCCGCTCTACTCAACAATAAT 304
QY 499 GGTGGATGATGCAACCTCTCTCCCAACACTTGCATGCTGAGCCTGCTTCTTCAA 558
DB 305 GGTGGTGGTGCATCTCTCTCCCAACACTTGTATTTAGACACACTGCTTCTTGCAA 364
QY 559 ATCGCTCAATACGAGCTGTATGCTCCCGCTCTCTCTGAGGGTACCATGATGAAG 618
DB 365 ATTGCTAATACAAAGCCGATGCTCCCTGTATCTTTTGAAGGGTCCCTGTATGAGA 424
QY 619 AAAGGTGAGTGAAGTTTACAATGAGCCACTCATCTTCAACTCGTTTGAATCACA 678
DB 425 AAAGGAGGATTAAGTTTACAGTAATGAGCACTCATTTTCAACTGTTTGTAGTACA 484
QY 679 AACGTGGTGGCGGACGCGACGCTCTGTGTCGATAAAGGGTCTGCACTGATGG 738
DB 485 AATGTTGAGGTGCTGTGATATTCATCAGTTCAATTAAAGGGTCTAATACTGATGG 544
QY 739 CAATCCATGTCTAGAAATTTGGGGCCAAAACCTGGCAAAAGCAAACTATCTCAATGGCCAA 798
DB 545 CAAGCAATGTCAAGATATTGGGGCCAAAATTTGGCAAAAGCAATCTAATCTATATGCTCAA 604
QY 799 GGCCTTTCCTTCAAGTCACTCTTAAGTATGATGCTGCACTCTCACTGCTATATACTCGTT 858
DB 605 AGTCTTTCATTTATGTCAACCAAGTATGAGGAGGACACTCATTTAGCAACAATGCTGCA 664
QY 859 CCTTCCAATTGGCAATTTGGCCAAACCTATGAAGGCCCTCAATTCTA 905
DB 665 CCAATTAATTGGCAATTTTGGACAACCTTTGAAGGGGCTCAATTTTA 711

RESULT 8
LOCUS CD484188 681 bp mRNA linear EST 04-JUN-2003
DEFINITION atr01-4msl-d02 Amborella trichopoda cDNA clone atr01-4msl-d02
5', mRNA sequence.
ACCESSION CD484188
VERSION CD484188.1 GI:31405456
KEYWORDS EST.
SOURCE Amborella trichopoda
ORGANISM Amborella trichopoda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE

1 (bases 1 to 681)
dePamphilis, C., Soltis, D., Soltis, P., Farmerie, W., Ma, H., Tanksley, S., Leebens-Mack, J., Field, D., Buzgo, M., Kim, S., Ilut, D., Landherr, L., Hu, Y., Wall, K., Albert, V., Carlson, J., Doyle, J., Frohlich, M., Miller, W., Oppenheimer, D. and Theissen, G.
Generation of ESTs from early flower buds of Amborella trichopoda

AUTHORS

TITLE

JOURNAL

Unpublished
Contact: Claude dePamphilis or James Leebens-Mack
Mueller Laboratory
Penn State University
208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
State University, University Park, PA 16802, USA
Tel: 814 863 6413
Fax: 814 865 9131

COMMENT

Email: cwd3@psu.edu or jhl10@psu.edu
The sequence provided is trimmed of vector and low quality regions.
Full sequence and original trace file are available from the Plant
Genome Network website (<http://pgn.cornell.edu>)
Plate: atr01-4msl row: d column: 02
Seq primer: M13F.

FEATURES

Location/Qualifiers
1..681
/organism="Amborella trichopoda"
/mol_type="mRNA"
/db_xref="taxon:13333"
/clone="atr01-4msl-d02"
/issue_type="flower buds"
/dev_stage="<= 2.5mm buds"
/lab_host="SOLR"
/clone_lib="atr01"

/note="Vector: pBluescript SK (+/-); Site 1: EcoRI;
Site 2: XhoI; Amborella trichopoda Baill; This library was
made from male flowers only. Only floral buds with
diameter of 2.5 mm or less were used for RNA isolation.
This is a directionally cloned, non-normalized library.
Avg. insert length: 1611; Primers: M13F and M13R;
Antibiotic: 50 ug/ml Ampicillin; Primary Titer: 2.24E6 pfu
total; Amplified Titer: 1.37E10 pfu/ml; Mass Excised
Titer: 3.53E9 total; This library has been generated by
the Floral Genome Project (FGP). We would like to thank
David Lorence at the National Tropical Botanical Garden
for providing plant material for library building. The
Floral Genome Project is funded by NSF's Plant Genome
Research Program (DBI-0115684). More information about the
project can be obtained at <http://fgp.bio.psu.edu>"

BASE COUNT

158 a 176 c 184 g 163 t

Query Match 41.5%; Score 411.4; DB 14; Length 681;
Best Local Similarity 77.4%; Pred. No. 7.8e-55;
Matches 499; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

QY 242 GCGGCCACGCCACCTTTATGAGTGTGTGACGATCTGCAACCATGAGTGGAGCTTGTG 301
DB 30 GCGGCCATGCCACATTTTATGAGTGTGTGATGCTACGGGACTATGCGGGAGCATGTG 89
QY 302 GGTATGGAAATTATACAGCCAAAGGATATGACGACGACGAGCGGCTGACCACTGGCC 361
DB 90 GATATGGAAATCTGTATAGCCAAAGGCTATGACGACGACGAGCGGCTGACCACTGCTC 149
QY 362 TATTTAACAATGATTAAGTGTGTGCTGCTTCTGAAATGACTGTACAACGACCCTA 421
DB 150 TCTTCAACGATGGCTTGAAGTGTGTCTCTGCTATGAATGAGGTGCAATGACGACCAA 209
QY 422 AATGTGCTCTCCGGAACTATTAGGCTCACTGCGACCAACTTTTGCCCTCTAATTG 481
DB 210 GGTGTGCTCTCCAGGCTCATTTGTGTCACTGCAACCAATTTCTGCCCCCAATTGG 269
QY 482 CTCTCCCTAACACAATGATGATGTGCAACCCCTCTTCCAAACACTTGCACATGCTG 541
DB 270 GTTTGCTAATGACAATGATGATGTGTGCAACCCCTCTTCCAAACACTTGTGACCTGCTG 329

QY 542 AGCTGCTTCTCTTCAATGCTCAATACCGAGCTGATCGTCCCGTCTCTTGTGTA 601
 Db 330 AACCTGCTTCTCTTCAATGCTCAATACCGAGCTGATCGTCCCGTCTCTTGTGTA 389
 QY 602 GGGTACCATGTATGAGAAAGGTGAGAGAGGTTTACATCAATGAGCACTCATCTTCA 661
 Db 390 GGATACCTGTGTGAGAAAGGTGAGATTAAGTTTACATCAATGAGCACTCATCTTCA 449
 QY 662 ACCCTGTTTGTATCAGAAAGCTGAGGCGCAGCGCAGCTCCTCTGTGTGATTAAG 721
 Db 450 ACTTGCTCTCATTAATGTAGTGGCGCGCGTGACATCCAGCGCGTGTCTCATTAAG 509
 QY 722 GGTCTGAACTGATGGCAATCCATGCTTAGAAATTTGGGCGCAAACTGCGCAAGCAACA 781
 Db 510 GATCCAAAGGTGATGGCAAGCCCATGCTCAGAACTGGGCGCAAACTGCGCAAGCAACA 569
 QY 782 ACTATCTCAATGGCCAGGCTTCTCTTCAAGTCACTCTTAGTGTGATGCTGCACTTCA 841
 Db 570 CCTACTCAATGGCCAGGCTTCTCTTCAAGTCACTCTTAGTGTGATGCTGCACTTCA 629
 QY 842 CTGCTTAATATCTGCTTCTTCAATTTGGCAATTTGGCCAAACCT 886
 Db 630 CAAGTTACAAAGTGGCGCTTCAATTTGGCAATTTGGCCAAACCT 674

RESULT 9
 BQ165503 786 bp mRNA linear EST 25-APR-2002
 LOCUS EST61372 KVVC Medicago truncatula cDNA clone pKVVC-9F12, mRNA
 DEFINITION sequence.

ACCESSION BQ165503
 VERSION BQ165503.1 GI:20307978
 KEYWORDS EST.
 SOURCE Medicago truncatula (barrel medic)
 ORGANISM Medicago truncatula

REFERENCE 1 (bases 1 to 786)
 VandenBosch, K., Endre, G., Silverstein, K., Town, C.D., Van Aken, S.,
 Utterback, T., Cheung, F. and Fraser, C.M.
 TITLE The Medicago truncatula 'kiloclone' set; ESTs selected and
 re-arrayed from various libraries
 JOURNAL Unpublished
 COMMENT Contact: VandenBosch K
 Department of Plant Biology
 University of Minnesota
 220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
 Tel: 612 624 2755
 Fax: 612 625 1738
 Email: kvandenb@chs.umn.edu
 TIGR sequence name: MTN172TK Alias Clone name: GVN-51C8 More
 information is available at: www.medicago.org
 Seq primer: SKmod (CTA GAA CTA gtc gat CC).

FEATURES
 source
 1..786

/organism="Medicago truncatula"
 /mol_type="mRNA"
 /cultivar="A17"
 /db_xref="taxon:3880"
 /clone="pKVVC-9F12"
 /tissue_type="mixed tissues"
 /dev_stage="various stages"
 /lab_host="XLOLR"
 /clone_lib="KVVC"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
 XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
 was directionally ligated into the Unizap XR vector from
 StrataGene and packaged using Gigapack III Gold packaging
 extracts. Plasmids containing cDNA inserts were excised
 from the recombinant lambda-Zap phage using Ex-assist

BASE COUNT 235 a 146 c 186 g 219 t
 ORIGIN
 helper phage and propagated in XLOLR cells."

Query Match 41.3%; Score 410; DB 13; Length 786;
 Best Local Similarity 78.2%; Pred. No. 1.2e-54;
 Matches 505; Conservative 0; Mismatches 140; Indels 1; Gaps 1;

QY 260 ATGGTGTGTGACGATCTGACCATGAGCTGTGGTATGGAATTATACA 319
 Db 1 ATGGTGAAGAGATGATCAGGCAATGGAGGCTGTGTTATGAAATTTGATA 60
 QY 320 GCCAAGGTATGGCAGAACACGCGCTGAGCAGCTGCGTTATTAACAATGATTA 379
 Db 61 GCCAAGGTATGGAACCAACACTGCTGACTAAGCACTGCTT-TTAACAATGATTA 119
 QY 380 GTTGCTGCTTGTCTGAAATGACTGTACAAAGCAACCTTAATGCTGCTTCCGGA 439
 Db 120 GTTGCTGCTTGTCTGAAATGACTGTACAAAGCAACCTTAATGCTGCTTCCGGA 179
 QY 440 CTATTAGGTCACGACCAACCTTTGCTTCACTTTGCTTCTTCAACAATG 499
 Db 180 GCAATTTGTTAGTACTGCTACAAACTTCTGCCCCCAACTTTGCAAGTCTAATACCAATG 239
 QY 500 GTGATGTGCAACCTCTCTTCAACACTTTCGACATGCTGAGCTGCTTCTTCAAA 559
 Db 240 GTGATGTGCAACCTCTCTTCAACACTTTCGACATGCTGAGCTGCTTCTTCAAA 299
 QY 560 TCGCTCAATACCGAGCTGTATGCTTCCCTCTTCTTCTGATGAGTACATGATGAGA 619
 Db 300 TTGCTCAATACCAAGCTGGAATGCTTCTTCTTCTGATGAGTACATGATGAGA 359
 QY 620 AAGTGAAGTGAAGTTTACATCAATGAGCCACTTCACTTCACTTCTTCTTCAACA 679
 Db 360 AAGTGAAGTGAAGTTTACATCAATGAGCCACTTCACTTCACTTCTTCTTCAACA 419
 QY 680 ACGTGTGCGCGCAGGCGAGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 739
 Db 420 ATGTTGTGAGAGCTGAGATGATGATGATGATGATGATGATGATGATGATGATG 479
 QY 740 AATCATGTGTAGAAATTTGGGCGCAAACTGCGCAACCACTATCTCAATGGCAAG 799
 Db 480 AAGCTATGTAGAAATTTGGGCGCAAACTGCGCAACCACTATCTCAATGGCAAG 539
 QY 800 GCGTTCTTCTTCAAGTCACTCTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 859
 Db 540 GCGTTCTTCTTCAAGTCACTCTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 599
 QY 860 CTTCAATTTGCAATTTGGCCAAACCTATGAAGCGCTCAATTTCA 905
 Db 600 CTTGCAATTTGCAATTTGGCCAAACCTATGAAGCGCTCAATTTCA 645

RESULT 10
 CA785153 719 bp mRNA linear EST 04-DEC-2002
 LOCUS sau25c03.y1 Gm-cl062 Glycine max cDNA clone SOYBEAN CLONE ID:
 DEFINITION Gm-cl062-9317 5' similar to TR:081133 081133 EXPANSIN.; mRNA
 sequence.

ACCESSION CA785153
 VERSION CA785153.1 GI:26048700
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max

REFERENCE 1 (bases 1 to 719)
 Shoemaker, R., Keim, P., Vodkin, L., Erpelidg, J., Coryell, V., Khanna,
 A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
 Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers,
 Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk

TITLE	JOURNAL	COMMENT
R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R..		
Public Soybean EST Project		
Unpublished		
Contact: Shoemaker R/Public Soybean EST Project		

Contact: Shemmaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 409.

FEATURES	Location/Qualifiers
source	1. .719

```

source
1. 719
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1062-9317"
/tissue_type="stem tissue of greenhouse grown plants"
/dev_stage="1 month old"
/lab_host="DH10B"
/clone_lib="Gm-c1062"
/note="Vector: Bluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from stem tissue of 1 month old greenhouse grown plants
for the cultivar Raiden. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the Bluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy Shoemaker."

```

Query Match	40.9%;	Score 406;	DB 14;	Length 719;
Best Local Similarity	78.4%;	Pred. No. 5.3e-54;		
Matches 500; Conservative	0;	Mismatches 135;	Indels 3;	Gaps 1;

OY	185	TCTTCTCTTCCTCCTTCTCTTTGTCTTCACTTCGCTGAATA--CGGTGGCTGGCAGA	241
Dd	79	TCTTCTCTTAATTTATGCTCCAGAGCACTTATGCTGACTAATGGAGGTGGCAAG	138
OY	242	GCGGCCACGCCACTTTTATGGTGSTGTGAACGATCTGGCACCATGGGTGAGCTTGTG	301
Dd	139	GTGTCATGCCACATTTTATGTGAGGTGATGCATCTGGACAATGGAGGGCTTGTG	198
OY	302	GGTATGGAAATTTATACAGCCAAGGTATGGACAAGAACGGTGGCGCTGAGCACTGGCG	361
Dd	199	GATATGGAATTTGTACAGCCCAAGGTATGGCACTAACACTGCAGCACTGACACTGCTC	258
OY	362	TATTTAACAATGGAATTAAGTTGTGTGCTTGCTTCGAATGACTTGTACAAAGACCCTA	421
Dd	259	TATTCAACATGGCATGAGTTGCGGGTCTTGCTATGAGATGAATGTGACACTGACCCCA	318
OY	422	AATGTGCTTCGCGGAACATAATGAGGTCACTGCCAACCACTTTTGGCCCTCAACTTTC	481
Dd	319	AATGTGCTTCGCGTAGCAATATCGTTACTGCCACAAACTTCTGCCCCCTTAACCTTTC	378
OY	482	CTCTCCCTAACACAATGTGGATGGTGC AACCTCCTCTCCAAACACTTGCACATGGCTG	541
Dd	379	CATTGGCTAACACAATGTGGCTGGTGC AACCCCTCTTGCAACACTTGAATCTTGCTG	438
OY	542	AGCCTGCCTTCCTCAAAATGCTCAATACCGAGCTGTATCGTCCCCTCTCCTTTCGTA	601
Dd	439	AGCCTGCTTTCCTTGCAAAATGCTCAATACAAAGCTGGAATGTTCAGATTTCTTCAGAA	498

QY	602	GGGTACCATGTATGAGAAGGAGTAGAGTTTACAATCAATAGGCCACTCATCTTCA	661
Db	499	GAGTCTCCTGTGTGAAGAAAGGAGGATCAGGTTCAACCATCAATGGTCACTTTACTTCA	558
QY	662	ACCTCGTTTGTGATCACAAACGTCGGTGGCGCGACGCTCACTCTGTGTGATAAAG	721
Db	559	ACTTGGTTTCATCACAAATGTTGGTGGAGCTGGAGATGTTCAATCTGTGTCCATCAAAG	618
QY	722	GGTCTCGAATCGATGGCAATTCATGTCCTAGAAATTGGGGCCAAACTGGCAAGCA	781
Db	619	GGTCTAGAACTGGGTGGCAAAACATGTCCTAGAACTGGGGGCGAGAAATTGGCAAGCACT	678
QY	782	ACTATCTCAATGGCCAAAGGCTTTCCTTTCAGTCACT	819
Db	679	CCTACCTGAATGGCCAAAGCCTCTCTTTTCAGTCACT	716

RESULT 11

LOCUS	CB822230	864 bp	mRNA	linear	EST 16-MAY-2003
DEFINITION	EST 3081 Half-Ripe Apricot Fruit Lambda Zap II Library Prunus armeniaca cDNA clone be05k06 3', mRNA sequence.				
ACCESSION	CB822230				
VERSION	CB822230.1	GI:29956247			
KEYWORDS	EST.				
SOURCE	Prunus armeniaca (apricot)				
ORGANISM	Prunus armeniaca				

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 864)	Grimplet, J., Romieu, C., Audergon, J. M., Albagnac, G., Lambert, P., Bouchet, J. P. and Terrier, N.	High Throughput Detection of Isogenes among 5724 3' EST from Apricot Fruit (<i>Prunus armeniaca</i>)

JOURNAL Unpublished
COMMENT Contact: Audergon JM

Unité de génétique et amélioration des fruits et légumes
Institut National de la Recherche Agronomique
Domaine Saint-Maurice BP 94 84143 Montfavet cedex
Tel: 00-33-(0)4-32-72-26-68
Fax: 00-33-(0)4-32-72-26-62
Email: audergon@avignon.inra.fr
Seq primer: T7.

FEATURES	Location/Qualifiers
Source	1. .864

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/organism="Prunus armeniaca"
/mol_type="mRNA"
/cultivar="Bergeron"
/db_xref="taxon:36596"
/clone="be005k06"
/dev_stage="Half-Ripe stage"
/clone_lib="Half-Ripe Apricot Fruit Lambda Zap II Library"
/note="Organ: Fruit; Vector: Lambda Zap II; Site_1: Eco RI
; Site_2: XhoI; Oriented library, construction described
in Molecular cloning and expression of a cDNA encoding
1-aminocyclopropane-1-carboxylate (ACC) oxidase from
apricot fruit (Prunus armeniaca cv. Bergeron) by
Mbeguie-Mbeguie D, Chahine H, Gomez RM, Gouble B, Audergon
JM, Souty M, Albagnac G, Fils-Lycaon B in Physiol Plant
105:294-303 1999"

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Query Match	40.8%;	Score 404.8;	DB 14;	Length 864;
Best Local Similarity	72.1%;	Pred. No. 7.5e-54;		
Matches 583; Conservative	0;	Mismatches 218;	Indels 8;	Gaps 4;

```

Qy      110 CCCACTTTTCTGCACAACTATTTTCAATATATAACCCATTCTTATGCGTTTCTTACT 169
          |||||  |||  |  |||||  |||||  |||||
Db      40 CCCATTCTTTCTCACACACAAAATATATACACACAATGGCTTTTACCTCACACTTAGC 99

```

[illegible]

COMMENT

Contact: Mikeal Roose
Department of Botany & Plant Sciences, University of California Riverside, CA, 92521-0124, USA
Tel: 9097874137
Fax: 9097874437
Email: mikeal.roose@ucr.edu
Seq primer: T7.

FEATURES

source	location/Qualifiers
	1..878
	/organism="Poncirus trifoliata"
	/mol_type="mRNA"
	/culivar="Pomeroy OP"
	/db_xref="taxon:37690"
	/clone="UCRPT01_01ae06"
	/tissue_type="phloem"
	/dev_stage="10 - 30 cm shoots"
	/lab_host="E. coli TJCl21"
	/clone_lib="Poncirus trifoliata CTV-challenged cDNA library - AGI"
	/note="Vector: lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse at University of California, Riverside. The scion was a open-pollinated (very probably selfed) seedling of Poncirus trifoliata cv Pomeroy that was selected as homozygous for the Ctv resistance gene. The rootstock was sweet orange infected with citrus tristeza virus (CTV) isolate TS14 over 1 year before sampling (CTV infects sweet orange, but not genotypes carrying the Ctv resistance gene. Shoots 10-30 cm long were harvested in October 2000, and the green phloem (bark) was removed and frozen quickly in dry ice. Total RNA was extracted using Trizol reagent (Gibco). Poly(A) RNA was purified, a cDNA library was made, and 0.5 million primary lambda cDNA clones were in vivo excised to give a population of pBluescript SK(-) phagemids. All steps to this point were performed in the ML Roose lab at the University of California, Riverside by X. Ye. Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3730 at the Arizona Genomics Institute, University of Arizona (Collura, Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files were transmitted to UC Riverside (by Y), then processed at UC Riverside (by Wanmaker) using th Harvest pipeline (http://harvest.ucr.edu) to remove vecto and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."

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BASE COUNT      235 a     223 c    182 g     238 t
ORIGIN
Query Match          40.8%; Score 404.6; DB 14; Length 878;
Best Local Similarity 76.8%; Pred. No. 8e-54;
Matches 494; Conservative 0; Mismatches 149; Indels 0; Gaps 0

QY       270 TGAGCATCTGGACACCATGTGTGAAGTTTGTGGTGTAAGAATTATAACGCCAAGGCTA   329
           ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
Db        878 TGATGCTTCGGCAACAATGGGTGTGTGGTGTAATGGAATTGTJACAGCCAAAGCCTA   819

QY       330 TTGCACGAACACCGGTGGCGCTGAGACTGCGCTATTAAACAATGATTAAGTTGTGTC   389
           ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
Db        818 TTGGACTAACACTGACGACTTAGTACCGCTCTATTCAAACAATAGGCTTAAGCTGTGCTC   759

QY       390 TTGCTTGAATGACTTGTAACAACGACCCTAAATGGTGCTTCGGGAACATATTAGGCT   449
           ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
Db        758 ATGCTATGAATGAATGTGAANAATGACCCCAAGTGGTGCTCCCCGGCTCATCATYTGT   699

QY       450 CATGCCACCAACTTTGGCCTCCTAACTTTGTGCTCCCTAACAACAATGGTGATGGTG   509
           ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
Db        698 CACGCCACCAACTTTGCCCACCACTTAACCTTGGCCCTGTCTAAGACAAACGGGGTTGGTG   639

QY       510 CAACCTCTCTCCAACACTTGGACATGGCTGAGCCTGCTCTCAATGCTCAATA   569
           ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
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Db	638	CAATCCTCCCCC	CCAGCACTTTG	CATGGCTG	AGCCCGCTTT	CTTGCAAAATTG	CCCAATA	579
QY	570	CCGAGCTG	TATCGTCCCCCG	CTCCTTT	CGTAGGGT	ACCATGTATG	AAGAAAGTGAGT	629
Dp	578	CCGTGCCG	TATCGTCCCA	TTTCTT	CAGAAGAT	CCCGTGTG	CGAAGAAAGAGAAT	519
QY	630	GAGGTTT	CAATCAATGG	CCACTCTA	TACTTCA	ACTCGTTT	TGATCACAAACGTCGGTG	689
Dp	518	AAGGTTT	ACCGTCAATG	GACACTCTA	CTTCACTT	CAACCTGGTTT	TGATCACAAATGTCGAGG	459
QY	690	CGCAGGCG	ACGTCAC	CTCTGTGTC	ATAAAGGGG	CTCGA	CTGGAATGGCAATCCATGTC	749
Dp	458	AGCAGGAG	ATGTGCAT	TTCAGTAT	CAATCAAGGGT	TTCAAGACTG	GATGGCAAGCAATGTC	399
QY	750	TAGAAATT	GGGGCCAAA	ACTGGCA	AGCAACA	CTATCTCA	ATGSGCCAAAGCCTTTCTT	809
Dp	398	AAGGA	ACTGGGGCC	CAAAATTGG	CGAGCAAT	TTCTTATCTTA	ACGGCCAAAGTCTTTCTT	339
QY	810	TCAAGT	CAC	CTTAGT	GTGTC	CACTCTCA	CTGCTTATATCTTCGTTCC	TTCCAATTG 869
Dp	338	CCAAGT	GACAGCC	AGTGA	CGGCG	AGCACTGT	GACTTAGCAACAATGTTGCTGC	TGGAAATTG 279
QY	870	GCAATTT	GGCCAA	CCATATG	AAAGCCCT	CAATTTCT	TAACCAT 912	
Dp	278	GCAATTT	GGGCAAA	CTTTG	AGGGTGT	CAAGTTT	TAGATTTTA 236	

RESULT 13	LOCUS	DEFINITION	ACCESSION	VERSION
BM780176	BM780176	770 bp mRNA linear EST 04-MAR-2002	ES1590764	KV2 Medicago truncatula cDNA clone pKV2-54C20, mRNA sequence.
	BM780176		BM780176	
	BM780176.1		GI:19110266	

SOURCE	Medicago truncatula (barrel medic)
ORGANISM	Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales; Medicago.

REFERENCE 1 (bases 1 to 770)

AUTHORS
Vandenbosch, K., Endre, G., Hur, J., Beremand, P., Town, C.D., Van Aken
, S., Utterback, T., Cheung, F., Tsai, J. and Fraser, C.M.

TITLE ESs from roots of *Medicago truncatula* 48 hr after inoculation with *Sinorhizobium meliloti*

JOURNAL Unpublished
COMMENT Contact: VandenBosch K

Department of Plant Biology
University of Minnesota
220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel.: 612 624 2755
Fax: 612 625 1738
Email: kvandenb@cs.umn.edu
TIGR sequence name: MTACV22TK More information is available at: www.medicago.org
Seq primer: Skmod (CTA gAA CTA gtg GAT CC).

FEATURES	location/Qualifiers
source	1. .770

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/organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pKV2-54C20"
/tissue_type="Seedling roots"
/dev_stage="2 days post-inoculation with Sinorhizobium
mellioti"
/lab_host="E. coli strain SOLR"
/clone_lib="KV2"
/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The
cDNA was directionally ligated into the Unizap XR vector
from Stratagene and packaged using Gigapack III Gold

```

BASE COUNT	214	a	164	c	169	g	223	t
ORIGIN	packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in SOLR cells."							

Query Match	40.7%;	Score 403.4;	DB 12;	length 770;
Best Local Similarity	76.7%;	Pred. No. 1.3e-53;		
Matches 507; Conservative	0;	Mismatches 151;	Indels 3;	Gaps 1;

[illegible]

RESULT 14	
BE131139	
LOCUS	815 bp mRNA linear
DEFINITION	L48-1090T3 Ice plant lambda Uni-Zap XR expression library, 48 hours NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-1090 5', mRNA sequence.
ACCESSION	BE131139
VERSION	BE131139.1
KEYWORDS	GI:8578502
SOURCE	EST.
ORGANISM	Mesembryanthemum crystallinum (common iceplant)
	Mesembryanthemum crystallinum
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Aizoaceae; Mesembryanthemum.

Query Match 40.5%; Score 401.8; DB 14; Length 736;
Best Local Similarity 77.3%; Pred. No. 2.4e-53;
Matches 486; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

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QY 229 GGTGGCTGGCAGACGGCCACGCACTTTTATGGTGGTGACGATCTGGCACCATG 288
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Db 108 GGAGGATGGCAAGGTGTCAACGCCCTTCAAGCGGTGTGATGCATCCGGCACATG 167
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 289 GGTGAGCTTGTGGTATGGGAATTATACAGCCAAGGTATGGCAGCAACGGTGGCG 348
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 168 GGAGGTGCTTGTGATATGTAATTATATAGCCAAGGTTGGGACCAACACAGACGA 227
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 349 CTGAGCACTGCGCTATTTAACAATGATTAAGTTGTGTGCTTCTCGAAATGACTGT 408
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 228 CTTAGCACTGCAATGTTTCAACAATGGGTGAGCTGTGTTCTTGTATGAATGAGTGT 287
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 409 ACAACGACCCCTAAATGSGCTTCCGGGAATTAAGGTCACTGCCACCACTTTTGC 468
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Db 288 GATGGTGACCCCAAAATGSGCTTGCCTGCTACCAATTAAGTCACTGCCACCAATTTTGT 347
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QY 469 CCTCCTAATTTGCTCTCCCAACAACAATGGTGGTGGCAACCTCCTCCCAACAC 528
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 348 CCCCCTAATTTGCTTGTCCAAATGATATAGTGGGTGGTGGCAACCTCCATTGCCAACAC 407
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QY 529 TTGCACATGGCTGAGCCTGCTTCTTCAATTCCTCAATACCGAGCTGTAATGTCCTCC 588
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Db 408 TTTGATTTGGCCGAGCCTGCTTCTTCAAAATAGCTCAATATCCGTGCTGGGATGTACCC 467
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QY 589 GTCTCCTTTCCGTAAGGTACCAATGATGAAGAAAGTGGAGTGGGTTACAATCAATGGC 648
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Db 468 GTTTCATTCAAGAGAGTCCCAATGATTAAGAAAGAGAGATCCGATTCAATCAACGGC 527
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 649 CACTCATCTTCAACCTCGTTTGATCACAACGTCGGTGGCGCAGCGACGTCCTCT 708
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Db 528 CACTCATCTTCAACTTGTCTTAATCACTAACGTTGGCGCGCCGAGATGTCCTCG 587
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QY 709 GTGTGATAAAGGGGTCTCGAACTGGATGGCAATCCATGTCTAGAAATTGGGGCCAAAAC 768
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Db 588 GTGTGATCAAGGGCTCGAAAAGTGGGTGGCAAGCAATGTCAAGGAAGTGGGGCCAGAAC 647
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QY 769 TGGCAAGCAACAATATCTCAATGGCAAGGCTTCTTCAAGTCACTCTTAGTGAT 828
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Db 648 TGGCAGAGCAACCTTACCTCAACGGCCAAACCTGTCTTCCAAGTCAACCAAGCGAT 707
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QY 829 GGTGCACTTCACTGCTATATCTGT 857
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Db 708 GGCAGAGCTTAACCAAGCTACACGTGT 736
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Search completed: December 18, 2003, 22:32:00
Job time : 2068 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 18, 2003, 19:52:30 ; Search time 3651 Seconds

(without alignments)
11115.407 Million cell updates/sec

Title: US-09-383-579C-9

Perfect score: 992
Sequence: 1 gaataaataacaacattgc.....aacacacaaacgcgaacgac 992

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_hcg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_hcg_hum:*

31: em_hcg_inv:*

32: em_hcg_other:*

33: em_hcg_mus:*

34: em_hcg_pln:*

35: em_hcg_rod:*

36: em_hcg_mam:*

37: em_hcg_vrt:*

38: em_sy:*

39: em_hugo_hum:*

40: em_hugo_mus:*

41: em_hugo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	992	100.0	992	8	CSU30382
2	684	69.0	684	6	AX306490
3	681	68.6	681	6	AR076514
4	681	68.6	681	6	AR161478
5	676.2	68.2	681	6	AX306492
6	453	45.7	1109	8	PAU93167
7	448.4	45.2	1177	8	AF049354
8	445.2	44.9	1153	8	AB093029
9	444.6	44.8	1243	8	AB093028
10	443.2	44.7	1118	8	AB093030
11	442	44.6	1109	8	AF350937
12	439.2	44.3	1048	8	AF297521
13	438.8	44.2	1035	8	CAR291817
14	435	43.9	1108	8	AY083166
15	431	43.4	1262	8	AY079206
16	429	43.2	1142	8	AF428174
17	428.6	43.2	1147	8	AF096776
18	424.2	42.8	1233	8	AF350936
19	423.6	42.7	1180	8	AF159563
20	421.8	42.5	1195	8	AB104444
21	420.6	42.4	1169	8	AY299692
22	420.2	42.4	1180	8	AB104443
23	417.8	42.1	1088	8	AF230332
24	416	41.9	1220	8	AB029083
25	415.2	41.9	1070	8	AY079208
26	412.6	41.6	1252	8	AF038815
27	409.2	41.2	1173	8	AF167360
28	405.6	40.9	1191	8	AY079205
29	404.4	40.8	1144	6	AX392019
30	401.8	40.5	1098	8	AY083168
31	401	40.4	1175	8	AB104445
32	398.8	40.2	1016	8	AY086770
33	394.2	39.7	762	6	AX506393
34	394.2	39.7	762	6	AX651951
35	390.2	39.3	740	6	AX654546
36	390.2	39.3	1219	8	OSU85246
37	388.6	39.2	1340	8	AB093031
38	388.2	39.1	1172	8	AF350938
39	387.6	39.1	1117	8	AF428175
40	386.2	38.9	1102	8	AF043284
41	386	38.9	756	6	AX653643
42	385.2	38.8	1323	8	OSU30477
43	383.8	38.7	1419	8	AF484847
44	383	38.6	1250	8	AY189969
45	382.6	38.6	891	8	PTU64893

ALIGNMENTS

RESULT 1

LOCUS CSU30382

DEFINITION Cucumis sativus expansin (Cs-Exp1) mRNA, complete cds.

ACCESSION U30382

VERSION U30382.1 GI:1040874

KEYWORDS

SOURCE Cucumis sativus (cucumber)

ORGANISM Cucumis sativus

REFERENCE 1 (bases 1 to 992)

AUTHORS Shcherban,T.Y., Shi,J., Durachko,D.M., Guiltinan,M.J., McQueen-Mason,S.J., Shieh,M. and Cosgrove,D.J.

cloning
seq 9

TITLE Molecular cloning and sequence analysis of expansins--a highly conserved, multigene family of proteins that mediate cell wall extension in plants

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 92 (20), 9245-9249 (1995)

MEDLINE 96016146

PUBMED 7568110

REFERENCE 2 (bases 1 to 992)

AUTHORS Shcherban,T., Shi,J., Durachko,D.M., Gultinan,M.J., McQueen-Mason,S.J., Shieh,M. and Cosgrove,D.J.

TITLE Direct Submission

JOURNAL Submitted (27-JUN-1995) Daniel J. Cosgrove, Biology, Pennsylvania State University, 208 Mueller Laboratory, University Park, PA 16802, USA

FEATURES

source location/Qualifiers

1..992

/organism="Cucumis sativus"

/mol_type="mRNA"

/strain="Burpee Pickler"

/db_xref="taxon:3659"

1..992

/gene="Cs-EXP1"

154..906

/gene="Cs-EXP1"

/note="similar to pollen allergen lol p1, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name Cuexs1; expansin-29 (Ex29) protein"

/codon_start=1

/product="expansin S1 precursor"

/protein_id="AAB37746.1"

/db_xref="GI:1040875"

/translation="MAFSYSPPSLFLPFEVFTFADYGMQSGHATFYGGDASGT MGACGYNLYSQGYGINTVALSTALFNNGLSCGACFEMCTNDPKMCLPGRIVTAT NCPNFPALPNNGWCMPLQHDMAEPALQIAQYRAGIVPSFRVFCMKKGVYR FTINGHSYFNLVLITNVGAGDVHSVSIKSRGTGWSMSRNMWQNNYLNQGLS FQVTLSDGRLLTAYNLVPSNMWQFGQTEGPQF"

223..903

/mat_peptide

/gene="Cs-EXP1"

/product="expansin S1"

/function="induces extension (creep) in plant cell walls"

992

/polyA_site

/gene="Cs-EXP1"

/note="17 A nucleotides"

BASE COUNT 259 a 277 c 177 g 279 t

ORIGIN

Query Match 100.0%; Score 992; DB 8; Length 992;

Best Local Similarity 100.0%; Pred. No. 2.5e-261;

Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATAATTACAACAATGGCACTAATTAATCTCATTTAATAACATTTCTTTTCGC 60

DB 1 GAATAATTACAACAATGGCACTAATTAATCTCATTTAATAACATTTCTTTTCGC 60

QY 61 TAATCTCCCTTTCTTCCCTCTTCTTCTTAACCCACAACCAACCCCACTTTCT 120

DB 61 TAATCTCCCTTTCTTCCCTCTTCTTCTTAACCCACAACCAACCCCACTTTCT 120

QY 121 TCACAACACTATTTCAAAATAAACCATTCTTATGCTTTTCTTACTCACCTTCTCC 180

DB 121 TCACAACACTATTTCAAAATAAACCATTCTTATGCTTTTCTTACTCACCTTCTCC 180

QY 181 TCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 240

DB 181 TCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 240

QY 241 AGCGGCACGCCACCTTTATGTGTGTGAGCATGTGGACCATGGGTGAGCTTGT 300

DB 241 AGCGGCACGCCACCTTTATGTGTGTGAGCATGTGGACCATGGGTGAGCTTGT 300

QY 301 GGGTATGGGAATTATACAGCCAAAGGTATGACGAAACAGGTGGCGCTGAGCATGGC 360

DB 301 GGGTATGGGAATTATACAGCCAAAGGTATGACGAAACAGGTGGCGCTGAGCATGGC 360

QY 361 CTAATTAACAATGATTAAGTTGTGTGCTTGCTTGCAAAATGACTGTGTACAAACGACCT 420

DB 361 CTAATTAACAATGATTAAGTTGTGTGCTTGCTTGCAAAATGACTGTGTACAAACGACCT 420

QY 421 AAATGTGCTTCGGGAACATTAAGGTCACTGACCCACCAACTTTTGCCTCTTAACCTT 480

DB 421 AAATGTGCTTCGGGAACATTAAGGTCACTGACCCACCAACTTTTGCCTCTTAACCTT 480

QY 481 GCTCTCCCTTAACAACAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540

DB 481 GCTCTCCCTTAACAACAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540

QY 541 GAGCCTGCTTCTTCAAAATGCTCAATACCGAGCTGTATCGTCCCGTCTCTTTCGT 600

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RESULT 2

AX306490

LOCUS AX306490 684 bp DNA linear PAT 11-DEC-2001

DEFINITION Sequence 1 from Patent WO0188163.

ACCESSION AX306490

VERSION AX306490.1 GI:17645710

KEYWORDS

SOURCE Cucumis sativus (cucumber)

ORGANISM Cucumis sativus

REFERENCE 1 Berendes,F., Raet,H.G., Vogt,U. and Gouloudis,C. Method for producing recombinant expansins Patent: WO 0188163-A 1 22-NOV-2001;

AUTHORS Bayer Aktiengesellschaft (DE)

TITLE

JOURNAL

FEATURES

source location/Qualifiers

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Db	629 ATCTCAATGGCCAGAGTCTTTCATTTCAAGTCACTCACTAGTGAATGGAAGGACTCTCACTA 688
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[illegible]

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QY	409	ACAAACGACCCTAAATGGTGGCTTCCGGGAACTAATTAGGGTCACTGCCACCAACTTTGC	468
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QY	469	CCTCCTAATTGTGCTCTCCCTAAACAACAATGGTGGATGGTGCAACCTCCTCTCCAACAC	528
Db	383	CCTCCCAACTTGGCGAGGCCAACAGACAATGGTGGCTGGTGCAACCTCCTCTCCAGCAC	442
QY	529	TTGCACATGGCTGAGCCTGCCTTCTTCAAAATGCTCAATACCGAGCTGGTATGCTCCC	588
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Db	563	CACCTTACTTCAACTTGGTTTGTATCAGCAAGCTCGGAGGACGAGACGTCCACTCT	622
QY	709	GTCGTGATAAAGGGTCTCGAAGCTGATGGCAATTCATGTCTAGAATTGGGGCCAAAC	768
Db	623	GTCGTGATCAAGGGTTCCAAGACAGGGTGGCAACCCCTGTCAAGAAATTGGGGCCAGAAC	682
QY	769	TGGCAAGCAACAACATATCTCAATGGCCCAAGCCTTTCCTTCAAGTCACTTTAGTGAT	828
Db	683	TGGCAGAGCAACTTACTTCAACGGCCAGAGCCTCTCCTTCCAGGTCAACCAACGAGAC	742
QY	829	GCTGCACTCTCACTGCTATATCTCGTTCCTTCCAATTTGGCAATTTGGCCAACTAT	888
Db	743	GGCAGAACTCTACCCGCCAACATATGTTGCCGCCGGAACCTGGCAGTTCCGACACAATTT	802
QY	889	GAAAGCCCTCAATTTTAAACCATATCAGCC	918
Db	803	GAGGGCAGTCAATTTCTGAGCTTCTCCGGC	832

RESULT	9
LOCUS	AB093028
DEFINITION	Pyrus communis PCExp1 mRNA for expansin, complete cds.
ACCESSION	AB093028
VERSION	AB093028.1 GI:29467498
KEYWORDS	
SOURCE	Pyrus communis (pear)
ORGANISM	Pyrus communis Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliopsida; eudicotyledons; core eudicots; rosids; eurosoids I; Rosales; Rosaceae; Maloideae; Pyrus.
REFERENCE	Hiwasa,K., Rose,J.K., Nakano,R., Inaba,A. and Kubo,Y. Differential expression of seven alpha-expansin genes during growth and ripening of pear fruit Unpublished
JOURNAL	2 (bases 1 to 1243)
REFERENCE	Hiwasa,K., Kubo,Y., Nakano,R. and Inaba,A.
AUTHORS	Direct Submission
TITLE	Submitted (08-OCT-2002) Kyoto Hiwasa, Okayama University, Graduate School of Natural Science and Technology, Tsushima-naka 1-1-1, Okayama, Okayama 700-8530, Japan (E-mail:k-hiwasa@cc.okayama-u.ac.jp, Tel:81-86-251-8338,
JOURNAL	Fax:81-86-251-8338)
FEATURES	
source	Location/Qualifiers 1..1243

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DB 187	GGAGTGCTTGTGATATGAAACTGTATAGTCAAGGGTACGGAACCAACTGCAGCA			246
QY 349	CTGAGCACTGCGCTATTTTAAACAATGATTAAGTTGTGTGCTTGTGAAATGACTTGT			408
DB 247	CTGAGCACAGCTCTCTTCAACGATGGCTTGAGCTGCGGTGCTGTATGAGATGAATGT			306
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QY 709	GTTGTGATAAAGGGGTCTCGAATGTGATGCAATCCATGTCTAGAAATGGGGCCAAAC			768
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QY 769	TGGCAAAAGCAACAATATCTCAATGAGCCAAAGCCTTCTTCAAGTCACTCTTAGTGAT			828
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QY 829	GGTGCATCTCTCACTGCGCTATAATCTCGTTCTTCCAAATGGCAATTTGGCCAAACCTAT			888
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	DEFINITION	Pyrus communis PCExp3 mRNA for expansin, complete cds.								
	ACCESSION	AB093030								
	VERSION	AB093030.1	GI:29467502							
	KEYWORDS									
	SOURCE									
	ORGANISM	Pyrus communis (pear)								
	AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Pyrus.								
	TITLE	Hiwasa,K., Rose,J.K., Nakano,R., Inaba,A. and Kubo,Y. Differential expression of seven alpha-expansin genes during growth and ripening of pear fruit								
	JOURNAL	Unpublished 2 (bases 1 to 1118) Hiwasa,K., Kubo,Y., Nakano,R. and Inaba,A.								
	REFERENCE	Submitted (08-OCT-2002) Kyoto Hiwasa, Okayama University, Graduate School of Natural Science and Technology; Tsushima-naka 1-1-1, Okayama, Okayama 700-8530, Japan (E-mail:k-hiwasa@cc.okayama-u.ac.jp, Tel:81-86-251-8338, Fax:81-86-251-8338)								
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Dd		232	TGGTTATGGGAATTTGTACAGCCAGGCGGTATGGAAACCAACACTGCAGCTTGAGCACAGC	291						
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Db	532	AAGATA	CACTTG	TGTGA	AGAAAG	AGGAAT	AAGATT	CAACCA	CGCCACT	CCCTACTT	591
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RESULT 11
AF350937
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
gene
CDS

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AF350937 1109 bp mRNA linear PLN 01-MAY-2001

Prunus cerasus expansin (EXP2) mRNA, complete cds.

AF350937

AF350937.1 GI:13898650

Prunus cerasus

Prunus cerasus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.

1 (bases 1 to 1109)

Yoo,S.-D., Gao,Z., Cantini,C., Loeschner,W. and van Nocker,S.

Coordinated expression of genes encoding expansins and other cell wall-modifying enzymes is associated with pectin-related changes in the cell wall during ripening of cherry (P. cerasus) fruit

Unpublished

2 (bases 1 to 1109)

Yoo,S.-D. and van Nocker,S.

Direct Submission

Submitted (19-FEB-2001) Department of Horticulture, Michigan State University, 392A Plant and Soil Science Building, East Lansing, MI 48824, USA

Location/Qualifiers

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QY	134	TCAATATATAAACCCATCTTATAGCGTTTTTCTTACTCACCCCTCTCTCTTCTTC	193			
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QY	732	TGATGGCAATCCATGTCTAGAAATTGGGGCCAAAACCTGGCAAGCAACAATATCTCAA	791			
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QY	852	TCTGTCTCTTCEAATTGGCAATTTGGCCAAACCTATGAAGGCCCTCAAATCTTAAACCAT	911			
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QY	912	ATCAGCCACACTGCTA 927				

Db 845 TTCCTAGATTATTA 860

RESULT 12
AF297521 1048 bp mRNA linear PLN 17-SEP-2000

LOCUS Prunus avium expansin 1 (Exp1) mRNA, complete cds.
DEFINITION AF297521
ACCESSION AF297521
VERSION AF297521.1 GI:10180016

KEYWORDS
SOURCE Prunus avium (sweet cherry)
ORGANISM Prunus avium
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
1 (bases 1 to 1048)
Wu, Z. and Wiersma, P.A.
REFERENCE Differential Expression of Expansin Genes Isolated from Sweet
AUTHORS Cherry (Prunus avium L.) During Fruit Ripening
TITLE Unpublished
JOURNAL 2 (bases 1 to 1048)
REFERENCE Wu, Z. and Wiersma, P.A.
AUTHORS Direct Submission
TITLE Submitted (18-AUG-2000) Agriculture and Agri-Food Canada, Pacific
JOURNAL Agri-Food Research Centre, 4200 Highway 97, Summerland, British
Columbia V0H 1Z0, Canada

FEATURES
source location/Qualifiers
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1..1048 /gene="Exp1"
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BASE COUNT 281 a 245 c 234 g 288 t

ORIGIN

Query Match 44.3%; Score 439.2; DB 8; Length 1048;
Best local Similarity 74.2%; Pred. No. 2.1e-109;
Matches 555; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

Db 180 CTCTCTCTTCTCTTCCTTCTCTTCTCTTCTCTCAACCTTCGCTGACTACCGGTGGCA 239
|||||
Db 119 CTCTCTTGTTCTCTTCAATCTTCACCTTCATGATGTCTTTTGCTGATTAATGTGGCTGGGA 178
|||||
Db 240 GAGCGGCCACGCCACCCTTTATAGTGCTGTCGACGCATCTGGCACCATGGGTGAGCTTG 299
|||||
Db 179 AGGGCGCTATGCCACTTTTATAGTGTCGCGGTGATGCTCCGGAAACAATGGGGGAGCATG 238
|||||
Db 300 TGGGTATGGGAATTATATACAGCCCAAGGATAATGGCAACAACGGGTGCGCTGAGCACTGC 359
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Db 239 TGGGTATGGGAATTATATACAGCCCAAGGATAATGGCAACAACGGGTGCGCTGAGCACTGC 298
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Db 360 GCTATTTAACATGATTAAGTGTGTGCTGCTGCTTGAATAATGACTTTGACAAACGACCCC 419
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Db 299 CTTGTTTAAACATGAGCTGTGGCTCTTGTATGAATAAGATGCAACAATGACCC 358
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Db 420 TAAATGTGCTTCGCGGAAGTATTAAGGCTCACTGCCCAACTTTGGCTCTTAATT 479
|||||
Db 359 TAGATGGTGTGCTCCGGAAGCATCATTTGTTACTGCTACAAACTTTGGCCCACTTAATT 418

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Db	419	TGCTCAGTCCAAACGATAAATGGCGGCTGGTGCAATCTCTCTCCAGCACTTTGATTTGGC	478
QY	540	TGAGCCTGCGCTTCTTCAAAATGCGTCAATACCGAGCTGGTATCGTCCCGTCTCTTTGG	599
Db	479	CGAGCCTGCTTCTTTCGAAATTTGCCCAATACCGCGCTGGGATTTGCTGTACCTTGAG	538
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QY	780	CAACTATCTCAATGGCCCAAGGCTTTCTTCAAGTCACTCTTAGTGATGGTGCACCTCT	839
Db	719	CACCTTACCTCAATGGCCAGAGCCCTCTCTTCCAAAGTGACCAACGATGACGAAGAATCTGT	778
QY	840	CACGCTCTATATCTCTCTTCCATTTGGCAATTTGGCCAAACCTATGAAGGCCCTCA	899
Db	779	CACAACTACAAACGTGGCCCCCTGGTAAATTTGGCAGTTTGGTCAGACTTTCTCAGGGGGGTCA	838
QY	900	ATTCTAAACCATATCAGCCACACTGCTA 927	
Db	839	ATTTAGAGTTATTCCACTAGATTATTA 866	

RESULT 13	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
CAR291817		CAR291817	1035 bp	MRNA	linear	PLN 19-DEC-2000	
		Cicer arietinum mRNA for expansin, clone CanExp-2.					
		AJ291817					
		AJ291817.1	GI:11932091				
		expansin.					
		Cicer arietinum (chickpea)					
		Cicer arietinum					
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Cicereae; Cicer.					
REFERENCE		1					
AUTHORS		Dopico, B., Sanchez, M.A. and Labrador, E.					
TITLE		An second expansin is expressed in chickpea epicotyls					
JOURNAL		Unpublished					
REFERENCE		2 (bases 1 to 1035)					
AUTHORS		Labrador, E.					
TITLE		Direct Submission					
JOURNAL		Submitted (15-DEC-2000) Labrador E., Dpto. Fisiologia Vegetal, Univ. Salamanca, Campus Miguel de Unamuno. Pza. Doctores de la Reina s/n, E-37007, SPAIN					
FEATURES		Location/Qualifiers					
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 BASE COUNT 312 a 168 c 213 g 342 t
 ORIGIN

Query Match	44.2%	Score 438.8;	DB 8;	Length 1035;
Best Local Similarity	77.2%	Pred. No. 2.7e-109;		
Matches 533; Conservative	0;	Mismatches 157;	Indels 0;	Gaps 0;

[illegible]

RESULT 14
 AY083166
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE

AY083166 1108 bp mRNA linear PLN 10-APR-2002
 Malus x domestica expansin 1 (EXP1) mRNA, complete cds.
 AY083166
 AY083166.1 GI:20135549

Malus x domestica (apple tree)
 Malus x domestica
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
 1 (bases 1 to 1108)

AUTHORS Trivedi, P.K. and Solomos, T.
TITLE Characterization of expansin cDNA from apple
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1108)
AUTHORS Trivedi, P.K. and Solomos, T.
TITLE Direct Submission
JOURNAL Submitted (08-MAR-2002) Department of Natural Resource Sciences and
Landscape Architecture, University of Maryland, College Park, MD
20742, USA

FEATURES
Source Location/Qualifiers
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BASE COUNT 317 a 250 c 243 g 297 t 1 others
ORIGIN

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Best Local Similarity 76.0%; Pred. No. 3e-108;
Matches 537; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 217 TTGCTGACTACGCTGGCTGGCAGAGCGGCCACCCCTTTATGTGTGGTGACGCA 276
DB 120 TTGGCTGTTATGCTAGCTGGGAGGCGCTTCATGCCACATTTACGCGCGGTGATGCC 179
QY 277 TCTGGACCATGGGTGAGCTTGTGGTATGGGAATTATACAGCCAAAGGTATGGCAGC 336
DB 180 TCGGCAACATGGGAGAGCATGTGTATGGGAATCTGTACAGCCAGGATATGGAACC 239
QY 337 AACACGGTGGCGCTGAGCAGCTGCGCTATTATCAATGATTAAGTGTGCTGCTTC 396
DB 240 AACACTGCAGCTTTGAGCAGACGATGTTCAACAATGGCTTGAGCTGTGATCTTGTAT 299
QY 397 GAAATGACTGTACAAACGACCTTAATGTGCTCCGGGAACTATTAGGCTCACTGCC 456
DB 300 GAAATGATGTCAACAATGACCCGAGATGTGCTGATCCATTATTGTACTGCT 359
QY 457 ACCAATTTTGGCTCTTAATCTTGTCTCCCTTAACAACAATGTGTGATGCAACCCCT 516
DB 360 ACAAACTTTGCTCTTAATCTTGTGATGCAACAACAATGTGTGATGCAATCCT 419
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QY 577 GGTATGCTCCCGTCTCTTCTGTAGGCTACATGATGAAGAGGTGAGTGGT 636
DB 480 GGAATGCTCCCGTCTCTTCTCAAGAAGTACCTGTATGAAGAAAGAGGATTAAGATTC 539
QY 637 ACAATCAATGGCCACTCATACCTCTTGTGATCAACAACGTGGTGGCGCAGGC 696
DB 540 ACCATCAAGCGCCACTCTCATCTTCAACCTGTTTGTATCAACAACGTGGTGGCAGGA 599
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QY 757 TGGGGCAAACTGGCAAGCAACAATATCTAATGCGCAAGCCTTCTTCAAGTC 816

DB 660 TGGGGTCAAACTGGCAGACCACTCATACTCAATGAGCCAGCCCTCTCTTCCAAATGTC 719
QY 817 ACTCTTAGTATGCTGGCAGCTCTCACTGCTATATCTGCTTCTTCCAAATGGCAATTT 876
DB 720 ACCACAGTACGCTAGTAACCGCTACAGACTTCAACGCTGCTCTGTATTTGGCAGTTT 779
QY 877 GGCCAACCTATGAGGCGCTCAATTTAAACCATATACGACCACT 923
DB 780 GGCAGACATTTCTCAGGGGGCAATTTAGAAATTATTCACCTAGACT 826

RESULT 15

AY079206 1262 bp mRNA linear PLN 15-APR-2003
LOCUS Mirabilis jalapa cell wall protein Exp4 precursor, mRNA, complete
DEFINITION cds.
ACCESSION AY079206
VERSION AY079206.1 GI:28624705
KEYWORDS
SOURCE Mirabilis jalapa (garden four o'clock)
ORGANISM Mirabilis jalapa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Nyctaginaceae; Mirabilis.

REFERENCE
AUTHORS Gookin, T.E., Hunter, D.A. and Reid, M.S.
TITLE Temporal analysis of alpha and beta-expansin expression during
floral opening and senescence
Plant Sci. 164 (5), 769-781 (2003)

JOURNAL
REFERENCE 2 (bases 1 to 1262)
AUTHORS Gookin, T.E., Hunter, D.A. and Reid, M.S.
TITLE Direct Submission
JOURNAL Submitted (19-FEB-2002) Department of Environmental Horticulture,
University of California, Davis, One Shields Avenue, Davis, CA
95616, USA

FEATURES
Source Location/Qualifiers
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76..834
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during senescence"
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ORIGIN

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Best Local Similarity 75.4%; Pred. No. 3.8e-107;
Matches 536; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

QY 202 TTCTTGTCTTACCTTGCTGACTAGCTGGCTGGCAGAGCGGCCACCCACTTTTAT 261
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QY 262 GGTGTGTGACGATCTGGACCATGGGTGAGCTTGTGGTATGGGAATTATACAGC 321
DB 190 GGTGAGAGATGCTTCTGGACCATGGGGGAGCTGTGATATGGGAATCTGTACAGT 249
QY 322 CAAGGTATGGACGAACAGGTGGCGCTGAGCACTGCCCTATTAAATGATTAAGT 381

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Db 370 ATAGTGTGACTGCAACCAATTTTGTCCACCTAATTAATGCTTAATTAACAATGT 429
QY 502 GGATGATGCAACCTCTCTCTCAACACTTGCACATGAGCTGAGCTGCTTCTTCAATC 561
Db 430 GGATGATGTAATCTCTCTCTCAACACTTGCACATGAGCTGAGCTGCTTCTTACAAAT 489
QY 562 GCTCAATACCGAGCTGTATGTCCTCCCTCTCTCTGTAGGGTACCATGTATGAAGAA 621
Db 490 GCTCAATACCGAGCTGTATGTCCTCCCTCTCTCTGTAGGGTACCATGTATGAAGAA 549
QY 622 GGTGAGTGAGGTTTACATCAATGAGCACTCATACTTCAACCTCGTTTGTATCACAAC 681
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Db 610 GTGGCGGAGCGCGGTGATGTCCATGAGTGTGATCAAGGGTCAAAAACCGGGTGGCAA 669
QY 742 TCCATGTCTAGAAATGGGGGCCAAAACCTGGCAAGCAACAATATCTCAATGGCCAAAGC 801
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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967.845 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 1107863

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1275	91.5	227	17	AAR94527
2	1275	91.5	227	23	AAG80768
3	1269	91.0	226	23	AAG80769
4	1131	81.1	223	23	ABB98474
5	1085	77.8	253	21	AAG25443
6	1085	77.8	253	21	AAG46483
7	1041	74.7	241	21	AAG06546
8	1041	74.7	241	21	AAG51633
9	1041	74.7	241	21	AAG51647

10	1041	74.7	249	21	AAG06545	Arabidopsis thalia
11	1041	74.7	249	21	AAG51632	Arabidopsis thalia
12	1041	74.7	249	21	AAG51646	Arabidopsis thalia
13	1041	74.7	259	21	AAG06544	Arabidopsis thalia
14	1041	74.7	259	21	AAG51631	Arabidopsis thalia
15	1041	74.7	280	21	AAG51645	Arabidopsis thalia
16	1030	73.9	228	23	AAG80771	N. tabacum expansi
17	1026.5	73.6	281	21	AAG43341	Arabidopsis thalia
18	1026	73.6	228	17	AAR94528	Rice expansin. Or
19	1024.5	73.5	282	21	AAG23850	Arabidopsis thalia
20	1024	73.5	251	21	AAG23852	Arabidopsis thalia
21	1024	73.5	251	21	AAG43343	Arabidopsis thalia
22	1024	73.5	253	21	AAG23851	Arabidopsis thalia
23	1024	73.5	253	21	AAG43342	Arabidopsis thalia
24	1002.5	71.9	227	17	AAR94532	Arabidopsis expans
25	999	71.7	250	22	AAE00414	Tomato seed expans
26	993	71.2	257	21	AAG36445	Arabidopsis thalia
27	970.5	69.6	207	21	AAG25444	Arabidopsis thalia
28	970.5	69.6	207	21	AAG46484	Arabidopsis thalia
29	970	69.6	241	21	AAG05453	Arabidopsis thalia
30	970	69.6	249	21	AAG05452	Arabidopsis thalia
31	970	69.6	255	21	AAG05451	Arabidopsis thalia
32	965	69.2	242	21	AAG36570	Arabidopsis thalia
33	965	69.2	249	21	AAG36569	Arabidopsis thalia
34	965	69.2	255	21	AAG36568	Arabidopsis thalia
35	962	69.0	225	17	AAR94531	Arabidopsis expans
36	944	67.7	262	21	AAG29931	Arabidopsis thalia
37	944	67.7	273	21	AAG29930	Arabidopsis thalia
38	939	67.4	255	21	AAG30325	Arabidopsis thalia
39	939	67.4	257	21	AAG30324	Arabidopsis thalia
40	938.5	67.3	258	23	AAE20570	Pear expansin 1 (E
41	934	67.0	250	21	AAG09622	Arabidopsis thalia
42	934	67.0	258	21	AAG09621	Arabidopsis thalia
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44	928	66.6	263	22	AAE00412	Tomato seed expans
45	895	64.2	210	21	AAG36446	Arabidopsis thalia

ALIGNMENTS

RESULT 1	
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ID AAR94527	standard; Protein; 227 AA.
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AC AAR94527;	
XX	
DT 25-MAR-2003	(updated)
DT 08-JUL-1996	(first entry)
XX	
DE	Cucumber expansin-29.
XX	
KW	Expansin-29; plant cell wall; cellulose; paper recycling; de-inking;
KW	polysaccharide; cucumber.
XX	
OS	Cucumis sativus var. Burpee Pickler.
XX	
PN	AU9540262-A.
XX	
PD	04-APR-1996.
XX	
PF	06-DEC-1995; 95AU-0040262.
XX	
PR	12-MAY-1993; 93US-0060944.
PR	12-MAY-1995; 95US-0440517.
PR	12-MAY-1994; 94AU-0068320.
XX	
PA	(PENN-) PENN STATE RES FOUND.
XX	
PI	Cosgrove DJ, McQueen-Mason S;
XX	
DR	WPI; 1996-201150/21.
DR	N-PSDB; AAT13320.

XX Expansin proteins which alter the mechanical strength of
PT poly:saccharide(s) - useful in paper mfr. and recycling
XX
PS Claim 7; Page 30; 60pp; English.
XX
CC Cucurber expansin-29 (AAR94527) is a member of a novel class of
CC proteins that catalyze the extension of plant cell walls and the
CC weakening of the hydrogen bonds in pure cellulose. It can be obtained
CC by expression of an isolated cDNA clone (see AAT13320) in bacterial or
CC other host cells. Expansin proteins have also been identified in oat
CC coleoptiles, in Arabidopsis (see AAR94530-32) and in rice (AAR94528-29),
CC and appear to be broadly distributed throughout the plant kingdom.
CC Expansins can be used e.g. in the mfr. of de-inking and recycling of
CC paper, in the textile industry, to aid delignification processes, to
CC alter gel mechanical strength, etc.
CC (Updated on 25-MAR-2003 to correct PR field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 227 AA;

Query Match 91.5%; Score 1275; DB 17; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.1e-118;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 DYGMQSGHATFYGGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSGACFEM 83
DB 1 DYGMQSGHATFYGGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSGACFEM 60
QY 84 TCTNDPKMCLPGTIRVTATNFCPPNPNALPNNNGWCNPPLOHFDMAEPALQIAQYRAGI 143
DB 61 TCTNDPKMCLPGTIRVTATNFCPPNPNALPNNNGWCNPPLOHFDMAEPALQIAQYRAGI 120
QY 144 VPVSFRRVPCMKKGGVRFRTINGHSYFNLVLTITNVGAGADVHSVSIKSRGTGQMSMRNWG 203
DB 121 VPVSFRRVPCMKKGGVRFRTINGHSYFNLVLTITNVGAGADVHSVSIKSRGTGQMSMRNWG 180
QY 204 QNMOSNNYLNGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPQF 250
DB 181 QNMOSNNYLNGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPQF 227

RESULT 2

AAAG80768
ID AAG80768 standard; Protein; 227 AA.
XX
AC AAG80768;
XX
DT 19-APR-2002 (first entry)
XX
DE C. sativus S1 expansin homologue fragment.
XX
KW Expansin; S1; cellulose-based textile; cotton; paper recycling;
XX paper pulp; plant tissue; papermaking; cucumber.
XX
OS Cucumis sativus.
XX
PN DE10032630-A1.
XX
PD 22-NOV-2001.
XX
PF 05-JUL-2000; 2000DE-1032630.
XX
PR 16-MAY-2000; 2000DE-1023561.
XX
PA (FARB) BAYER AG.
XX
PI Berendes F, Rast HG, Vogt U, Gouloudis C;
XX WPI; 2002-155755/21.
DR N-PSDB; ABA97161.
XX
PT Vector encoding an expansin, useful in treatment of cellulosic

PT materials for paper recycling, providing large-scale production -
XX
PS Example 1; Page 11-14; 22pp; German.
XX
CC This invention describes a novel vector (A) comprising (i) nucleic acid
CC (I) encoding an expansin (II) and (ii) coupled sequences that allow
CC expression of (I) in microorganisms. The recombinant expansins described
CC in the invention are used in preparation, treatment and finishing of
CC cellulose-based textiles (e.g. cotton) or in recycling of paper or for
CC preparation of pulp from plant tissue, as a substitute for corrosive
CC chemicals currently used in papermaking. Recombinant methods make
CC possible large scale production of extensin possible. This sequence
CC represents the Cucumis sativus (cucumber) S1 extensin homologue fragment
CC described in the invention.
XX
SQ Sequence 227 AA;

Query Match 91.5%; Score 1275; DB 23; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.1e-118;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 DYGMQSGHATFYGGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSGACFEM 83
DB 1 DYGMQSGHATFYGGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSGACFEM 60
QY 84 TCTNDPKMCLPGTIRVTATNFCPPNPNALPNNNGWCNPPLOHFDMAEPALQIAQYRAGI 143
DB 61 TCTNDPKMCLPGTIRVTATNFCPPNPNALPNNNGWCNPPLOHFDMAEPALQIAQYRAGI 120
QY 144 VPVSFRRVPCMKKGGVRFRTINGHSYFNLVLTITNVGAGADVHSVSIKSRGTGQMSMRNWG 203
DB 121 VPVSFRRVPCMKKGGVRFRTINGHSYFNLVLTITNVGAGADVHSVSIKSRGTGQMSMRNWG 180
QY 204 QNMOSNNYLNGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPQF 250
DB 181 QNMOSNNYLNGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPQF 227

RESULT 3

AAAG80769
ID AAG80769 standard; Protein; 226 AA.
XX
AC AAG80769;
XX
DT 19-APR-2002 (first entry)
XX
DE C. sativus expansin cseexpla fragment.
XX
KW Expansin; cellulose-based textile; cotton; paper recycling; cseexpla;
XX paper pulp; plant tissue; papermaking; cucumber.
XX
OS Cucumis sativus.
XX
PN DE10032630-A1.
XX
PD 22-NOV-2001.
XX
PF 05-JUL-2000; 2000DE-1032630.
XX
PR 16-MAY-2000; 2000DE-1023561.
XX
PA (FARB) BAYER AG.
XX
PI Berendes F, Rast HG, Vogt U, Gouloudis C;
XX WPI; 2002-155755/21.
DR N-PSDB; ABA97162.
XX
PT Vector encoding an expansin, useful in treatment of cellulosic
XX materials for paper recycling, providing large-scale production -
PS Example 1; Page 14-16; 22pp; German.
XX

CC This invention describes a novel vector (A) comprising (i) nucleic acid
 CC (I) encoding an expansin (II) and (ii) coupled sequences that allow
 CC expression of (I) in microorganisms. The recombinant expansins described
 CC in the invention are used in preparation, treatment and finishing of
 CC cellulose-based textiles (e.g. cotton) or in recycling of paper or for
 CC preparation of pulp from plant tissue, as a substitute for corrosive
 CC chemicals currently used in papermaking. Recombinant methods make
 CC possible large scale production of extensin possible. This sequence
 CC represents the Cucumis sativus (cucumber) extensin, csepla, fragment
 CC described in the invention.

XX Sequence 226 AA;

Query Match 91.0%; Score 1269; DB 23; Length 226;
 Best Local Similarity 100.0%; Pred. No. 1.2e-117;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 DYGMQSGHATFYGGDASGTWGCAGCYGNLYSQGYGTNTVALSTALFNNNGISCGACFEM 83
 DB 1 DYGMQSGHATFYGGDASGTWGCAGCYGNLYSQGYGTNTVALSTALFNNNGISCGACFEM 60
 QY 84 TCTNDPKWCLPGTIRVTATNCPNPFALPNNNGWCNPPLOHFDMAEPALQIAQYRAGI 143
 DB 61 TCTNDPKWCLPGTIRVTATNCPNPFALPNNNGWCNPPLOHFDMAEPALQIAQYRAGI 120
 QY 144 VPVSFRRVPCMKKGGVRFITNGHSYFNLVLTNVGAGDVHSVSIKGSRTGQMSMRNWG 203
 DB 121 VPVSFRRVPCMKKGGVRFITNGHSYFNLVLTNVGAGDVHSVSIKGSRTGQMSMRNWG 180
 QY 204 QNMOSNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTEGPQ 249
 DB 181 QNMOSNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTEGPQ 226

RESULT 4

ABB98474 standard; Protein; 223 AA.

XX ABB98474;
 AC ABB98474;
 XX 01-NOV-2002 (first entry)
 DE Plant expansin consensus sequence.
 XX
 KW Longibrachiatum; filamentous fungus; swollenin; cotton fibre swelling;
 KW cellulose; cellulosic substrate; animal food; biomass; glucose;
 KW paper manufacture; laundry detergent; plant; expansin.
 XX

OS Unidentified.

XX US2002086350-A1.

PN 04-JUL-2002.

XX 09-JUL-1998; 98US-0112498.

XX 11-JUL-1997; 97US-0893766.

PA (SWAN/) SWANSON B A.
 PA (WARD/) WARD M.
 PA (PENT/) PENTTILA M.
 PA (JAAK/) JAAKO P.
 PA (SALO/) SALOHEIMO M.

PI Swanson BA, Ward M, Penttila M, Jaako P, Saloheimo M;

DR WPI; 2002-642241/69.

XX Novel swollenin protein isolated from fungus or bacteria, has
 PT applications in cleaning textiles (laundry detergents and pre-wash
 PT compositions), modifying textiles (depilling, color restoration,
 PT anti-greying) -
 XX

PS Example 1; Fig 2; 20pp; English.

XX The present invention relates to swollenin from Trichoderma reesei
 CC (Longibrachiatum, a filamentous fungus). Swollenins facilitate weakening
 CC of filter paper and the swelling of cotton fibres without having
 CC cellulolytic activity i.e., catalytic activity involving the breakage of
 CC individual cellulose strands into smaller monomer (glucose) or oligomers
 CC (polysaccharides). Swollenin and its coding sequence are useful in
 CC methods for altering the properties of cellulosic substrate. Preferably
 CC the methods are useful for altering the nutritional properties of animal
 CC feed, altering the properties of fabric or yarn comprising cellulosic
 CC fibres, altering properties of cellulosic biomass during its reduction to
 CC glucose, altering properties of wood pulp or its derivatives during paper
 CC manufacture, and altering properties of cellulosic corn husk fibre during
 CC its reduction to glucose. The swollenin coding sequence has utility in
 CC many applications for which cellulase is currently used, for example,
 CC cleaning textiles (laundry detergents and pre-wash compositions),
 CC modifying textiles (depilling, colour restoration, anti-greying), and
 CC improvement of the nutritive value of animal feeds. Since the swollenin
 CC coding sequence is expressed by a fungus, it can be produced in large
 CC quantities. The present sequence is a consensus sequence for plant
 CC expansin, which was used in a sequence alignment with a partial swollenin
 CC protein sequence. It was found that there was a 21.7% identity between
 CC the sequences.

XX Sequence 223 AA;

Query Match 81.1%; Score 1131; DB 23; Length 223;
 Best Local Similarity 88.4%; Pred. No. 5.9e-104;
 Matches 199; Conservative 16; Mismatches 8; Indels 2; Gaps 2;

QY 26 GGMQSGHATFYGGDASGTWGCAGCYGNLYSQGYGTNTVALSTALFNNNGISCGACFEMTC 85
 DB 1 GGMQSAHATFYGGDASGTWGCAGCYGNLYSQGYGTNTVALSTALFNNNGISCGACFELTC 60
 QY 86 TNDPKWCLPGTIRVTATNCPNPFALPNNNGWCNPPLOHFDMAEPALQIAQYRAGI 145
 DB 61 DNDPKWCLPGSITVTATNCPNPFALPNNNGWCNPPLOHFDMAEPALQIAQYRAGI 120
 QY 146 VSFRVPCMKKGGVRFITNGHSYFNLVLTNVGAGDVHSVSIKGSRTGQMSMRNWG 205
 DB 121 VAYRRVPCMKKGGVRFITNGHSYFNLVLTNVGAGDVHSVSIKGSRTGQMSMRNWG 180
 QY 206 WQSNMYLNQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTEGPQ 250
 DB 181 WQSNMYLNQGLSFQVTLSDGRTVTS-NVAPANMQFGQTF-GGQF 223

RESULT 5

AAG25443 standard; Protein; 253 AA.

XX AAG25443;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 29510.

XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0130449.
 PR 23-APR-1999; 99US-0130510.
 PR 28-APR-1999; 99US-0130891.
 PR 30-APR-1999; 99US-0131449.
 PR 30-APR-1999; 99US-0132048.
 PR 04-MAY-1999; 99US-0132407.
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 PR 06-MAY-1999; 99US-0132485.
 PR 06-MAY-1999; 99US-0132486.
 PR 07-MAY-1999; 99US-0132487.
 PR 11-MAY-1999; 99US-0132863.
 PR 14-MAY-1999; 99US-0134256.
 PR 14-MAY-1999; 99US-0134218.
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 PR 14-MAY-1999; 99US-0134370.
 PR 18-MAY-1999; 99US-0134768.
 PR 19-MAY-1999; 99US-0134941.
 PR 20-MAY-1999; 99US-0135124.
 PR 21-MAY-1999; 99US-0135353.
 PR 24-MAY-1999; 99US-0135629.
 PR 25-MAY-1999; 99US-0136021.
 PR 27-MAY-1999; 99US-0136392.
 PR 28-MAY-1999; 99US-0136782.
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 PR 03-JUN-1999; 99US-0137528.
 PR 04-JUN-1999; 99US-0137502.
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 PR 18-JUN-1999; 99US-0139763.
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 PR 22-JUN-1999; 99US-0139899.
 PR 23-JUN-1999; 99US-0140353.
 PR 23-JUN-1999; 99US-0140354.
 PR 24-JUN-1999; 99US-0140695.
 PR 28-JUN-1999; 99US-0140823.
 PR 29-JUN-1999; 99US-0140991.
 PR 30-JUN-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141842.
 PR 01-JUL-1999; 99US-0142154.
 PR 02-JUL-1999; 99US-0142055.
 PR 06-JUL-1999; 99US-0142390.
 PR 08-JUL-1999; 99US-0142803.
 PR 09-JUL-1999; 99US-0142920.
 PR 12-JUL-1999; 99US-0142977.
 PR 13-JUL-1999; 99US-0143542.
 PR 14-JUL-1999; 99US-0143624.
 PR 15-JUL-1999; 99US-0144005.

PR 16-JUL-1999; 99US-0144085.
 PR 16-JUL-1999; 99US-0144086.
 PR 19-JUL-1999; 99US-0144325.
 PR 19-JUL-1999; 99US-0144331.
 PR 19-JUL-1999; 99US-0144332.
 PR 19-JUL-1999; 99US-0144333.
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 PR 21-JUL-1999; 99US-0145086.
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 PR 22-JUL-1999; 99US-0145085.
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 PR 22-JUL-1999; 99US-0145089.
 PR 22-JUL-1999; 99US-0145192.
 PR 23-JUL-1999; 99US-0145145.
 PR 23-JUL-1999; 99US-0145218.
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 PR 26-JUL-1999; 99US-0145276.
 PR 27-JUL-1999; 99US-0145913.
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 PR 27-JUL-1999; 99US-0145919.
 PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
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 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 23-AUG-1999; 99US-0150566.
 PR 25-AUG-1999; 99US-0150564.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.

PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 77.8%; Score 1085; DB 21; Length 253;
Best Local Similarity 77.9%; Pred. No. 2.6e-99;
Matches 194; Conservative 22; Mismatches 31; Indels 2; Gaps 2;

QY 4 SYSPFSSFLPLPFFV-FTPADYGMQSGHATFYGGDASGTMGACGYGNLYSQGYGTN 62
Db 5 SYLKYSIISIISVLFLOGTHGDDGWMQGGHATFYGGEDASGTMGACGYGNLYSQGYGTN 64
QY 63 TVALSTALFNNGLSGACFEMTCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGWCNPP 122
Db 65 TAAALSTALFNNGLTGACYEMKCNDDPRWCLGSTITVTATNFCPPNPGLSNDNGWCNPP 124
QY 123 LQHFDMABPAFLQIAQYRAGIVPSFRFRVPCMKKGVRFTINGHSYFNLVLITNVGAGD 182
Db 125 LQHFDLAEPALQIAQYRAGIVPSFRFRVPCMKKGIRFTINGHSYFNLVLISNVGAGD 184
QY 183 VHSVSIKSGRT-GWQMSRNMWQNMQSNVYNGQLSFQVTLSDGRTLTAYNLVPSNMQF 241
Db 185 VHAVSIKSGRTQSWQMSRNMWQNMQSNVYNDQSLSFQVTTSDGRTLVSNDVAPSNMQF 244
QY 242 GQTYEGPOF 250
Db 245 GQTYQGQOF 253

RESULT 6

AA646483
ID AAG46483 standard; Protein; 253 AA.

XX AAG46483;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 58485.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

OS

PN EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
PF 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
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PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
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PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
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PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.

PR	01-JUL-1999;	99US-0142154.
PR	02-JUL-1999;	99US-0142055.
PR	06-JUL-1999;	99US-0142390.
PR	08-JUL-1999;	99US-0142803.
PR	09-JUL-1999;	99US-0142920.
PR	12-JUL-1999;	99US-0142977.
PR	13-JUL-1999;	99US-0143542.
PR	14-JUL-1999;	99US-0143624.
PR	15-JUL-1999;	99US-0144005.
PR	16-JUL-1999;	99US-0144085.
PR	16-JUL-1999;	99US-0144086.
PR	19-JUL-1999;	99US-0144325.
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4 SYSPFSLFLIPFFV-FTPADYGWGSGHATFYGGDASGTMGCAGYNLYSQGYGTN 62
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Dd

5 SYLKYSIISLIVLFLOCTHGDDCGWOGGHATFYGGEDASGTMGCAGCYGNLYGOGYGTN 64

QY	63	TVA	STAL	FNNGL	SCAC	FE	MT	CTND	BK	WCL	P	G	T	I	R	A	T	N	F	C	P	N	F	A	L	P	N	N	G	M	C	N	P	122			
Db	65	TAA	STAL	FNNGL	TCAC	YEM	K	C	N	D	P	R	W	C	L	S	T	I	T	A	T	N	F	C	P	P	N	F	G	I	S	N	D	N	G	M	C

QY	123	125	1822
123	LQHEDMAEPALQIAQYRAGIVPVSFRRVPCMKKGVRFTINGHSYFNLVLITNVGAGD		
Db	125	LQHEDMAEPALQIAQYRAGIVPVSFRRVPCMKKGGRFTINGHSYFNLVLISNVGAGD	1844

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QY      183 VHASVIKGSRT-GWQSMSRNWGQNQNSNNYLNGQGSLFQVLTSDGRITLAVNLPSPNQOF 2411  
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Db      185 VHAIVIKGSKTQSWAMSRNWGNQNSNSYNDQSLSFQVTTSDGRITLVSNDAVPSPNQOF 2444
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QY	242	GQTYEGPQF	250
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Db	245	GQTYOGGQF	253

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AC	AAG06546;
XX	
DT	17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 3357.
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XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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DT 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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Qy      206 WQSNNYLNGQLSFQVTLSDGRFTLAYNLVPSNMQFGQTYEGPQF 250
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Db 196 WQNSNYLNGQALSFKVTTS DGRVVSFNAPAGWSTYGQTFAGGQF 240

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AC AAG51647;

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DT 18-OCT-2000 (first entry)

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KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

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OS Arabidopsis thaliana.

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KW hybridisation assay; genetic mapping; gene expression control; promoter;
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Best Local Similarity 79.6%; Pred. No. 5.9e-95;
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DB 24 GGMWNAHATFYGGDASGTMGACGCGNLYSQGYGTSTALSTALFNNGLSCGSCFEIRC 83

QY 86 TNDPKWCLEPTIRVTATNFCPPNFALPNNNGWCNPLOHFDMAEPALQIAYRAGIVP 145
DB 84 ENDGKWCLEPGSIVVTATNFCPPNFALPNNNGWCNPPLHFDLAQPVFORIAYRAGIVP 143
QY 146 VSFRRVPCMKKGVRFTINGHSYENLVLTITVVGAGDVHSVSIKGSRTGWQSMRRWGON 205
DB 144 VSYRRVPCRRRGIRFTINGHSYENLVLTITVVGAGDVHSAAIKGSRTVWQAMSRWGON 203
QY 206 WQSNMYLNGGSLSFQVTLSDGRTLTAYNLVPSPNWQFGQTYEGPOF 250
DB 204 WQSNXYLNGQALSFKVTTSDDRTVVSFNAAAPAGWSYQOTFAGQOF 248
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AC AAG51632;
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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Db		84	ENRGKMCPLPGSIVVTATNFCCPPNNALLANNNGMGCNPLEHFDLAQPVFORIAQYRAGIVP	1433
QY		146	VSERRRVPCMKKGVRFTINGHSYFNVLITNVGAGADVHSVSIKGSRTQMOSMRNWGN	205
Db		144	VSYRRVPCRRRRGGIIRFTINGHSYFNVLITNVGAGADVHSAIKGSRTYWQAMSRNWGN	2033
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XX	DT	18-OCT-2000	(first entry)	
XX	DE	Arabidopsis thaliana protein fragment SEQ ID NO: 65569.		
XX	KX	Protein identification; signal transduction pathway; metabolic pathway;		
KW		hybridisation assay; genetic mapping; gene expression control; promoter;		
KW		termination sequence.		
XX	OS	Arabidopsis thaliana.		
XX	PN	EP1033405-A2.		
XX	PD	06-SEP-2000.		
XX	PF	25-FEB-2000; 2000EP-0301439.		
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PR 29-OCT-1999; 99US-0162142.
Query Match 74.7%; Score 1041; DB 21; Length 249;
Best Local Similarity 79.6%; Pred. No. 5.9e-95;
Matches 179; Conservative 23; Mismatches 23; Indels 0; Gaps 0;

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OY 86 TNDPKWCLPGTIRVTATNFCPPNFPALPNNNGWCNPPLQHFDMABEFLQIAQYRAGIIV 145
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OY 146 VSFRRVPCMKKGAVFTINGHSYFNLVLTNMGAGDVHSVSIKSRGTGQMSRWGQN 205
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DB 144 VSYRRVPCRRRGIRFTINGHSYFNLVLTNMGAGDVHSAAIKSRTVWQAMSRWGN 203

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AC AAG06544;
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DT 17-OCT-2000 (first entry)
XX
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XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
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DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 65568.

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hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

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PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.

PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.

PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 74.7%; Score 1041; DB 21; Length 280;
Best Local Similarity 79.6%; Pred. No. 6.9e-95;
Matches 179; Conservative 23; Mismatches 23; Indels 0; Gaps 0;

QY 26 GGNQSGHATFYGGDASGTMGACGYGNLYSGGYGTNTVALSTALFNNGLSCGACFEMTC 85
||| : |||||
Db 55 GGNINAHATFYGGDASGTMGACGYGNLYSGGYGTSTALSTALFNNGLSCGSCFEIRC 114
||| : |||||
QY 86 TNDPKWCLPGTIRVTATNFCPPNFALPNNNGWCNPPLOHFDMAEPALQIAQYRAGIYP 145
||| : |||||
Db 115 ENDGKWCPLPGSIVTATNFCPPNNALANNNGWCNPPLEHFDLAQPVFORIAQYRAGIYP 174
||| : |||||
QY 146 VSPRRVPCMKKGVRFTINGHSYFNLVLITNVGAGADVHSVSIKGSRTGWQSMRWNQON 205
||| : |||||
Db 175 VSYRRVPCRRRGIRFTINGHSYFNLVLITNVGAGADVHSALIKGSRTVWQAMSRWNQON 234
||| : |||||
QY 206 WQSNMYLNGGGLSFQVTLSDGRITLTAYNLVPSPWQFGQTYEGPOF 250
||| : |||||
Db 235 WQSNMYLNGGGLSFQVTLSDGRITVVSFNAAPAGWSYGQTFAGGOF 279
||| : |||||

Search completed: December 18, 2003, 17:48:29
Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 17:47:38 ; Search time 21 Seconds
(without alignments)
503.701 Million cell updates/sec

Title: US-09-383-579C-10
Perfect score: 1394
Sequence: 1 MAFSISPFSSLFLLPFRFVF.....AYNLVPSNMQFGQTYEGPQF 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cg2_6/ptodata/1/iaa/5B_COMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1275	91.5	227	4	US-09-112-498A-5 Sequence 5, Appli
2	1265	90.7	227	3	US-09-092-160-7 Sequence 7, Appli
3	1131	81.1	223	4	US-09-112-498A-3 Sequence 3, Appli
4	1035	74.2	233	4	US-09-112-498A-11 Sequence 11, Appl
5	1032	74.0	237	4	US-09-112-498A-7 Sequence 7, Appli
6	1026	73.6	228	2	US-08-440-517A-2 Sequence 2, Appli
7	1026	73.6	228	3	US-09-092-160-2 Sequence 2, Appli
8	1022.5	73.4	232	4	US-09-112-498A-8 Sequence 8, Appli
9	1011.5	72.6	226	2	US-08-440-517A-6 Sequence 6, Appli
10	1011.5	72.6	226	3	US-09-092-160-6 Sequence 6, Appli
11	962	69.0	225	2	US-08-440-517A-5 Sequence 5, Appli
12	962	69.0	225	3	US-09-092-160-5 Sequence 5, Appli
13	939	67.4	241	4	US-09-112-498A-10 Sequence 10, Appl
14	937	67.2	258	4	US-09-112-498A-13 Sequence 13, Appl
15	889.5	63.8	233	4	US-09-112-498A-9 Sequence 9, Appli
16	884	63.4	234	4	US-09-112-498A-6 Sequence 6, Appli
17	857.5	61.5	222	2	US-08-440-517A-3 Sequence 3, Appli
18	857.5	61.5	222	3	US-09-092-160-3 Sequence 3, Appli
19	841.5	60.4	225	4	US-09-092-160-2 Sequence 2, Appli
20	839.5	60.2	225	2	US-08-445-539-2 Sequence 2, Appli
21	825.5	59.2	233	4	US-09-112-498A-12 Sequence 12, Appl
22	797	57.2	179	2	US-08-845-539-6 Sequence 6, Appli
23	797	57.2	179	4	US-09-362-642-6 Sequence 6, Appli
24	773.5	55.5	227	2	US-08-440-517A-4 Sequence 4, Appli
25	773.5	55.5	227	3	US-09-092-160-4 Sequence 4, Appli
26	732	52.5	167	2	US-08-845-539-4 Sequence 4, Appli
27	732	52.5	167	4	US-09-362-642-4 Sequence 4, Appli

28	248.5	17.8	261	1	US-07-971-096-2 Sequence 2, Appli
29	248.5	17.8	261	1	US-08-175-096-2 Sequence 2, Appli
30	239	17.1	263	4	US-09-811-672-10 Sequence 10, Appl
31	236	16.9	246	3	US-08-441-507-21 Sequence 21, Appl
32	236	16.9	246	4	US-07-969-875A-21 Sequence 21, Appl
33	234	16.8	272	3	US-08-441-507-15 Sequence 15, Appl
34	234	16.8	272	4	US-07-969-875A-15 Sequence 15, Appl
35	233	16.7	263	1	US-07-971-096-4 Sequence 4, Appli
36	233	16.7	263	1	US-08-175-096-4 Sequence 4, Appli
37	233	16.7	263	3	US-08-413-974-6 Sequence 6, Appli
38	233	16.7	263	3	US-08-434-418-6 Sequence 6, Appli
39	233	16.7	263	3	US-08-433-288-6 Sequence 6, Appli
40	233	16.7	263	3	US-08-174-739A-6 Sequence 6, Appli
41	233	16.7	263	4	US-08-434-256-6 Sequence 6, Appli
42	207	14.8	245	3	US-08-441-507-24 Sequence 24, Appl
43	207	14.8	245	4	US-07-969-875A-24 Sequence 24, Appl
44	173	12.4	197	3	US-08-441-507-5 Sequence 5, Appli
45	173	12.4	197	4	US-07-969-875A-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-112-498A-5
; Sequence 5, Application US/09112498A
; Patent No. 6458928
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MICROBIAL SWOLLENIN PROTEIN, DNA SEQUENCES
; TITLE OF INVENTION: ENCODING SUCH SWOLLENINS AND METHOD OF PRODUCING SUCH
; TITLE OF INVENTION: SWOLLENINS
; NUMBER OF SEQUENCES: 31
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/112,498A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 98/14226
; FILING DATE:
; APPLICATION NUMBER: US 08/893,766
; FILING DATE: 11-JUL-1997
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-112-498A-5

Query Match 91.5%; Score 1275; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 8.7e-117;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 DYGSWGSHATFYGGDASGTMGACGYNLYSGYGTNTVALSTALFNNGLSGACPFEM 83
DB 1 DYGSWGSHATFYGGDASGTMGACGYNLYSGYGTNTVALSTALFNNGLSGACPFEM 60
QY 84 TCTNDPKCLPGTIRVTATNFCPPNFPALPNNNGWCNPPLOHFDMAEPAFLQIAQYRAGI 143
DB 61 TCTNDPKCLPGTIRVTATNFCPPNFPALPNNNGWCNPPLOHFDMAEPAFLQIAQYRAGI 120
QY 144 VPVSFRVRPCMKKGAVFTINGHSYFNLVLTNVGAGDVHSVSIKSGRTGQMSMRWG 203
DB 121 VPVSFRVRPCMKKGAVFTINGHSYFNLVLTNVGAGDVHSVSIKSGRTGQMSMRWG 180
QY 204 QNMOSNNYLNGLSPQVTLSDGRTLTAYNLVPSNMQFGQTYEGPQF 250
DB 181 QNMOSNNYLNGLSPQVTLSDGRTLTAYNLVPSNMQFGQTYEGPQF 227

RESULT 2

US-09-092-160-7
; Sequence 7, Application US/09092160C
; Patent No. 6255466
; GENERAL INFORMATION:
; APPLICANT: Cosgrove, Daniel J
; APPLICANT: McQueen-Mason, Simon
; APPLICANT: Guiltinan, Mark J
; APPLICANT: Shcherban, Tatyana
; APPLICANT: Shi, Jun
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; FILE REFERENCE: 1194/1C114US3
; CURRENT APPLICATION NUMBER: US/09/092,160C
; EARLIER FILING DATE: 1998-06-05
; EARLIER FILING DATE: 1995-05-12
; EARLIER FILING DATE: 1994-05-12
; EARLIER FILING DATE: 1994-05-12
; EARLIER FILING DATE: 1993-05-12
; EARLIER FILING DATE: 1993-05-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cucumber
; OTHER INFORMATION: expansin
US-09-092-160-7

Query Match 90.7%; Score 1265; DB 3; Length 227;
Best Local Similarity 99.1%; Pred. No. 8.3e-116;
Matches 225; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 24 DYGMQSGHATFYGGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEM 83
DB 1 DYGMQSGHATFYGGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEM 60
QY 84 TCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGWCNPLOHFDMAEPALQIAQYRAGI 143
DB 61 TCTNDPKWCLPGTIRVTATNFCPPNFALPNDGWCNPLOHFDMAEPALQIAQYRAGI 120
QY 144 VPSFRVPCKMKGGVRFITNGHSYFNLVLITNVGAGDVHSVSIKSGRTGWSMRNWG 203
DB 121 VPSFRVPCKMKGGVRFITNGHSYFNLVLITNVGAGDVHSVSIKSGRTGWSMRNWG 180
QY 204 QNMOSNNYLGQGLSFQVTLSDGRITLTAYNLVPSPNQFGQTYEGPOF 250
DB 181 QNMOSNNYLGQGLSFQVTLSDGRITLTAYNLVPSPNQFGQTYEGPOF 227

RESULT 3

US-09-112-498A-3
; Sequence 3, Application US/09112498A
; Patent No. 6458928
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MICROBIAL SWOLLENIN PROTEIN, DNA SEQUENCES
; TITLE OF INVENTION: ENCODING SUCH SWOLLENINS AND METHOD OF PRODUCING SUCH
; TITLE OF INVENTION: SWOLLENINS
; NUMBER OF SEQUENCES: 31
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/112,498A
; FILING DATE:
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 98/14226
; FILING DATE:
; APPLICATION NUMBER: US 08/893,766
; FILING DATE: 11-JUL-1997
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-112-498A-3

Query Match 81.1%; Score 1131; DB 4; Length 223;
Best Local Similarity 88.4%; Pred. No. 9.9e-103;
Matches 199; Conservative 16; Mismatches 8; Indels 2; Gaps 2;

QY 26 GGMQSGHATFYGGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC 85
DB 1 GGMQSAHATFYGGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFELTC 60
QY 86 TNDPKWCLPGTIRVTATNFCPPNFALPNNNGWCNPLOHFDMAEPALQIAQYRAGI 145
DB 61 DNDPKWCLPGSITVTATNFCPPNFALPNNNGWCNPLOHFDMAEPALQIAQYRAGI 120
QY 146 VPSFRVPCKMKGGVRFITNGHSYFNLVLITNVGAGDVHSVSIKSGRTGWSMRNWGON 205
DB 121 VAYRVPCKKRGIRFTINGHSYFNLVLITNVGAGDVHSVSIKSGRTGWSMRNWGON 180
QY 206 WQSNYYLNGQGLSFQVTLSDGRITLTAYNLVPSPNQFGQTYEGPOF 250
DB 181 WQSNYYLNGQGLSFQVTLSDGRITVTS-NVAPANWQFGQTF-GGQF 223

RESULT 4

US-09-112-498A-11
; Sequence 11, Application US/09112498A
; Patent No. 6458928
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MICROBIAL SWOLLENIN PROTEIN, DNA SEQUENCES
; TITLE OF INVENTION: ENCODING SUCH SWOLLENINS AND METHOD OF PRODUCING SUCH
; NUMBER OF SEQUENCES: 31
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/112,498A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 98/14226
; FILING DATE:
; APPLICATION NUMBER: US 08/893,766
; FILING DATE: 11-JUL-1997
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-112-498A-11

Query Match 74.2%; Score 1035; DB 4; Length 233;
Best Local Similarity 78.1%; Pred. No. 2.5e-93;
Matches 178; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 23 ADYGWQSGHATFYGGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFE 82
DB 6 ADYGWQSAHATFYGGGDASGTMGACGYGNLYSTGYGTNTAALSTVLFNDGAACRSCYE 65
QY 83 MTCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGWCNPLOHFDMAEPALQIAQYRAG 142

TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 226
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis
US-09-092-160-6

Query Match 72.6%; Score 1011.5; DB 3; Length 226;
Best Local Similarity 77.1%; Pred. No. 4.7e-91;
Matches 175; Conservative 23; Mismatches 28; Indels 1; Gaps 1;

QY 24 DYGMQSGHATFYGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSGACFEM 83
DB 1 DYSSWQSAHATFYGGDASGTMGTCGYGNLYSTGY-TNTALSTVLFNDAACRSCYEL 59
QY 84 TCTNDPKWCLPGTIRVTATNFCBPNFALPNNNGWCNPPLOHFDMAEPALQIAQYRAGI 143
DB 60 RCDNDGQWCLPGSVTVATNLCBPNYALPNDGWCNPPRPHFDMAEPALQIGVYRAGI 119
QY 144 VPVSFRVRPCMKKGVRFTINGHSYFNVLITNVGAGDVHSVSIKGSRTGQMSRNMW 203
DB 120 VPVSFRVRPCMKKGIRFTINGHSYFNVLITNVGAGDVHSVSIKGSRTGQMSRNMW 179
QY 204 QNMQSNNTYLNQGLSFQVTLSDGRTLTAYNLVPSNMWQFGQTYEGPOF 250
DB 180 QNMQSNNTYLDGQSLSFQVAVSDGRTVTSNNVPAWQFGQTYEGGQF 226

RESULT 11
US-08-440-517A-5
Sequence 5, Application US/08440517A
Patent No: 5959082
GENERAL INFORMATION:
APPLICANT: COSGROVE, DANIEL J.;
APPLICANT: GUILTINAN, MARK;
APPLICANT: SHCHERBAN, TATYANA;
APPLICANT: SHI, JUN
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
STREET: 113 TECHNOLOGY CENTER
CITY: UNIVERSITY PARK
STATE: PENNSYLVANIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 16802-7000
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,517A
FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 225

TYPE: AMINO ACID
TOPOLOGY: UNKNOWN
US-08-440-517A-5

Query Match 69.0%; Score 962; DB 2; Length 225;
Best Local Similarity 75.0%; Pred. No. 3.2e-86;
Matches 171; Conservative 26; Mismatches 27; Indels 4; Gaps 2;

QY 24 DYGMQSGHATFYGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSGACFEM 83
DB 1 DNGWMERGHATFYGGADASGTMGACGYGNLHSGYGLQFALSTALFNSGKCGACFEL 60
QY 84 TCTNDPKWCLPGTIRVTATNFCBPNFALPNNNGWCNPPLOHFDMAEPALQIAQYRAGI 143
DB 61 TCEDDPEWCIPGSIIV--RYNLANFALANDNGWCNPPKHFDAEPALQIAQYRAGI 117
QY 144 VPVSFRVRPCMKKGVRFTINGHSYFNVLITNVGAGDVHSVSIKGSRTG-QMSRNMW 202
DB 118 VPVAFRRVRPCMKKGIRFTINGNPFYFDLITNVGAGDIAVSLKSKTDQWQMSRNMW 177
QY 203 QNMQSNNTYLNQGLSFQVTLSDGRTLTAYNLVPSNMWQFGQTYEGPOF 250
DB 178 QNMQSNNTYLRGQSLSFQVTLSDGRTVSVYDVPDHWQFGQTYEGGQF 225

RESULT 12
US-09-092-160-5
Sequence 5, Application US/09092160C
Patent No. 6255466
GENERAL INFORMATION:
APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 225
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis
US-09-092-160-5

Query Match 69.0%; Score 962; DB 3; Length 225;
Best Local Similarity 75.0%; Pred. No. 3.2e-86;
Matches 171; Conservative 26; Mismatches 27; Indels 4; Gaps 2;

QY 24 DYGMQSGHATFYGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSGACFEM 83
DB 1 DNGWMERGHATFYGGADASGTMGACGYGNLHSGYGLQFALSTALFNSGKCGACFEL 60
QY 84 TCTNDPKWCLPGTIRVTATNFCBPNFALPNNNGWCNPPLOHFDMAEPALQIAQYRAGI 143
DB 61 TCEDDPEWCIPGSIIV--RYNLANFALANDNGWCNPPKHFDAEPALQIAQYRAGI 117
QY 144 VPVSFRVRPCMKKGVRFTINGHSYFNVLITNVGAGDVHSVSIKGSRTG-QMSRNMW 202
DB 118 VPVAFRRVRPCMKKGIRFTINGNPFYFDLITNVGAGDIAVSLKSKTDQWQMSRNMW 177
QY 203 QNMQSNNTYLNQGLSFQVTLSDGRTLTAYNLVPSNMWQFGQTYEGPOF 250

Db 178 GQNWQNTYLRGQSLSFQVTDSDGRITVSYDVVPHDMQFGQTFEGGQF 225

RESULT 13

US-09-112-498A-10
Sequence 10, Application US/09112498A
Patent No. 6458928

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: MICROBIAL SWOLLENIN PROTEIN, DNA SEQUENCES

TITLE OF INVENTION: ENCODING SUCH SWOLLENINS AND METHOD OF PRODUCING SUCH

TITLE OF INVENTION: SWOLLENINS

NUMBER OF SEQUENCES: 31

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/112,498A

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 98/14226

FILING DATE:

APPLICATION NUMBER: US 08/893,766

FILING DATE: 11-JUL-1997

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 241 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-09-112-498A-10

Query Match 67.4%; Score 939; DB 4; Length 241;
Best Local Similarity 70.9%; Pred. No. 6.2e-84;
Matches 161; Conservative 29; Mismatches 35; Indels 2; Gaps 1;

QY 26 GQWQSGHATFYGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSGACFEWTC 85

Db 13 GQWETAHATFYGGSDASGTMGACGYGNLYSQGYGTNTALSTALFNNGFSGACFELKC 72

QY 86 TNDPKWCLPG--TIRVTATNFCPPNFALPNNNGWCNPPLOHFDMAEPALQIAQYRAGI 143

Db 73 ASDPKWCHSGSPSIFITATNFCPPNFAQPSDNGWCNPPRPHFDLAMPFLKIAEYRAGI 132

QY 144 VPVSFRRVPCMKKGAVRFTINGHSYFNVLITNVGAGDVHSVSIKSGRTGQMSRHWG 203

Db 133 VPVSFRRVPCMKKGAVRFTINGHSYFNVLITNVGAGDVHSVSIKSGRTGQMSRHWG 192

QY 204 QNWQSNVYLVGQSLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPOF 250

Db 193 QNWQSNVYLVGQSLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPOF 239

RESULT 14

US-09-112-498A-13
Sequence 13, Application US/09112498A
Patent No. 6458928

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: MICROBIAL SWOLLENIN PROTEIN, DNA SEQUENCES

TITLE OF INVENTION: ENCODING SUCH SWOLLENINS AND METHOD OF PRODUCING SUCH

TITLE OF INVENTION: SWOLLENINS

NUMBER OF SEQUENCES: 31

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/112,498A

FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 98/14226

FILING DATE:

APPLICATION NUMBER: US 08/893,766

FILING DATE: 11-JUL-1997

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 258 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-09-112-498A-13

Query Match 67.2%; Score 937; DB 4; Length 258;
Best Local Similarity 72.7%; Pred. No. 1.1e-83;
Matches 165; Conservative 21; Mismatches 39; Indels 2; Gaps 1;

QY 26 GQWQSGHATFYGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSGACFEWTC 85

Db 30 GQWETAHATFYGGSDASGTMGACGYGNLYSQGYGTNTALSTALFNNGFSGACFELKC 89

QY 86 TNDPKWCLPG--TIRVTATNFCPPNFALPNNNGWCNPPLOHFDMAEPALQIAQYRAGI 143

Db 90 DQDPRWCNPNPSILITATNFCPPNFAEPSDNGWCNPPRPHFDLAMPFLKIAQYRAGI 149

QY 144 VPVSFRRVPCMKKGAVRFTINGHSYFNVLITNVGAGDVHSVSIKSGRTGQMSRHWG 203

Db 150 VPVAYRRVPCMKKGAVRFTINGHSYFNVLITNVGAGDVHSVSIKSGRTGQMSRHWG 209

QY 204 QNWQSNVYLVGQSLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPOF 250

Db 210 QNWQSNVYLVGQSLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPOF 256

RESULT 15

US-09-112-498A-9
Sequence 9, Application US/09112498A
Patent No. 6458928

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: MICROBIAL SWOLLENIN PROTEIN, DNA SEQUENCES

TITLE OF INVENTION: ENCODING SUCH SWOLLENINS AND METHOD OF PRODUCING SUCH

TITLE OF INVENTION: SWOLLENINS

NUMBER OF SEQUENCES: 31

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/112,498A

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 98/14226

FILING DATE:

APPLICATION NUMBER: US 08/893,766

FILING DATE: 11-JUL-1997

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 233 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-09-112-498A-9

Query Match 63.8%; Score 889.5; DB 4; Length 233;
Best Local Similarity 69.5%; Pred. No. 4e-79;
Matches 157; Conservative 26; Mismatches 34; Indels 9; Gaps 2;

QY 26 GQWQSGHATFYGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSGACFEWTC 85

Db 14 GQWETAHATFYGGSDASGTMGACGYGNLYSQGYGTNTALSTALFNNGFSGACFELKC 73

QY 86 TNDPKWCLPG-TIRVTATNFCPPNFALPNNNGWCNPLOHFDMAEPALQIAQYRAGIV 144
Db 74 VNDPQWCICKRSIVVTATNFCPP-----GGACDPNNHHFDLSQPIYEKIALYKSGII 125
QY 145 PVSFRVRVPCMKKGVRFTINGHSYFNVLITNVGAGDVHSVSIKSRGTGWSMRNWQ 204
Db 126 PVMYRRVRCKRSGGIRFTINGHSYFNVLITNVGAGDVHSVSMKGSRTKQMLMSRNWQ 185
QY 205 NWQSNMYLNGQGISFOVTLSDGRTLTAYNLVPSPNWQFGQTYEGPQF 250
Db 186 NWQSNMYLNGQGISFOVTLSDGRTLTAYNLVPSPNWQFGQTYEGPQF 231

Search completed: December 18, 2003, 17:50:54
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 17:49:54 ; Search time 32 Seconds

(without alignments)
1459.052 Million cell updates/sec

Title: US-09-383-579C-10

Perfect score: 1394

Sequence: 1 MAFSYPFSSFLPLPPFVF.....AYNLVPSNMQFGQTYEGPQF 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1265	90.7	227	10	US-09-896-301-7 Sequence 7, Appli
2	1228	88.1	225	15	US-10-197-294A-6 Sequence 6, Appli
3	1131	81.1	223	15	US-10-197-294A-4 Sequence 4, Appli
4	1109.5	79.6	222	15	US-10-197-294A-5 Sequence 5, Appli
5	1044	74.9	258	12	US-10-150-559-4 Sequence 4, Appli
6	1035	74.2	233	15	US-10-197-294A-12 Sequence 12, Appli
7	1027	73.7	253	12	US-10-409-701-9 Sequence 9, Appli
8	1026	73.6	228	10	US-09-896-301-2 Sequence 2, Appli
9	1017.5	73.0	236	15	US-10-197-294A-8 Sequence 8, Appli
10	1013.5	72.7	232	15	US-10-197-294A-9 Sequence 9, Appli
11	1011.5	72.6	226	10	US-09-896-301-6 Sequence 6, Appli
12	962	69.0	225	10	US-09-896-301-5 Sequence 5, Appli
13	940	67.4	241	15	US-10-197-294A-11 Sequence 11, Appli
14	937	67.2	237	15	US-10-197-294A-14 Sequence 14, Appli
15	889.5	63.8	233	15	US-10-197-294A-10 Sequence 10, Appli

16	884	63.4	234	15	US-10-197-294A-7 Sequence 7, Appli
17	857.5	61.5	222	10	US-09-896-301-3 Sequence 3, Appli
18	814	58.4	232	15	US-10-197-294A-13 Sequence 13, Appli
19	773.5	55.5	227	10	US-09-896-301-4 Sequence 4, Appli
20	362.5	26.0	247	15	US-10-125-001-20 Sequence 20, Appli
21	302.5	21.7	299	15	US-10-125-001-22 Sequence 22, Appli
22	294	21.1	308	15	US-10-125-001-4 Sequence 4, Appli
23	273	19.6	245	15	US-10-125-001-14 Sequence 14, Appli
24	266.5	19.1	282	12	US-10-102-349-2 Sequence 2, Appli
25	266.5	19.1	282	12	US-10-102-349-4 Sequence 4, Appli
26	266.5	19.1	282	15	US-10-125-001-2 Sequence 2, Appli
27	262.5	18.8	265	15	US-10-125-001-12 Sequence 12, Appli
28	253.5	18.2	239	12	US-10-259-165-276 Sequence 276, App
29	246	17.6	283	12	US-10-409-701-11 Sequence 11, Appli
30	239	17.1	263	9	US-09-811-672-10 Sequence 10, Appli
31	239	17.1	263	11	US-09-847-208-138 Sequence 138, App
32	236.5	17.0	240	9	US-09-949-888-2 Sequence 2, Appli
33	232.5	16.7	265	11	US-09-847-208-107 Sequence 107, App
34	232	16.6	231	15	US-10-125-001-11 Sequence 11, Appli
35	229	16.4	263	11	US-09-847-208-112 Sequence 112, App
36	220.5	15.8	269	11	US-09-847-208-133 Sequence 133, App
37	206.5	14.8	222	12	US-10-259-165-44 Sequence 44, Appli
38	206.5	14.8	222	12	US-10-259-165-392 Sequence 392, App
39	192.5	13.8	263	11	US-09-847-208-127 Sequence 127, App
40	185.5	13.3	190	15	US-10-125-001-13 Sequence 13, Appli
41	185	13.3	191	11	US-09-847-208-173 Sequence 173, App
42	150.5	10.8	322	15	US-10-197-294A-3 Sequence 3, Appli
43	150.5	10.8	493	15	US-10-197-294A-2 Sequence 2, Appli
44	109.5	7.9	138	15	US-10-125-001-19 Sequence 19, Appli
45	100.5	7.2	54	12	US-10-161-660-12 Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-09-896-301-7
; Sequence 7, Application US/09896301
; Patent No. US20020103355A1
; GENERAL INFORMATION:
; APPLICANT: Cosgrove, Daniel J
; APPLICANT: McQueen-Mason, Simon
; APPLICANT: Guiltinan, Mark J
; APPLICANT: Shcherban, Tatyana
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; FILE REFERENCE: 1194/1C114US3
; CURRENT APPLICATION NUMBER: US/09/896,301
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/092,160
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 08/440,517
; PRIOR FILING DATE: 1995-05-12
; PRIOR APPLICATION NUMBER: 08/242,090
; PRIOR FILING DATE: 1994-05-12
; PRIOR APPLICATION NUMBER: 08/060,944
; PRIOR FILING DATE: 1993-05-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cucumber
; OTHER INFORMATION: expansin
; US-09-896-301-7

Query Match 90.7%; Score 1265; DB 10; Length 227;
Best Local Similarity 99.1%; Pred. No. 2.4e-118;
Matches 225; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 24 DYCGWQSGHATFYGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEM 83

Dy

1 DYGGWQSGHATFYGGGDSAGTMGACGCYGNLYSQYGINTVALSTALFNNGLSGACFEM 60

QY

84 TCTNDPKMCLPGTIRVATA TNFCPPNFALPNNNGWCNPLPHFDMAEPALFOIAQYRAGI 143
||||| : |||||
61 TCTNDPKMCLPGTIRVATA TNFCPPNFALPNDGGM CNPLPHFDMAEPALFOIAQYRAGI 120

Dy

144 VPSFRVP PCMKKGV RFTINGHSY FNLVLITNVGAGADVHSYSIKSRTGMSMRNWG 203
|||||
121 VPVSFRVRPCMKKGV RFTINGHSY FNLVLITNVGAGADVHSYSIKSRTGMSMRNWG 180

QY

204 QNMGSNNYLNGQGLSFQVYTLSDGR TLTAAYNLVPSNMQFGQTYEGPOF 250
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181 QNMGSNNYLNGQGLSFQVYTLSDGR TLTAAYNLVPSNMQFGQTYEGPOF 227

Dy

RESULT 2

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: Sequence 6, Application US/10197294A
: Publication No. US20030104546A1
: GENERAL INFORMATION:
: APPLICANT: Swanson, Barbara A.
: APPLICANT: Ward, Michael
: APPLICANT: Penttila, Merja
: APPLICANT: Pere, Jaakko
: APPLICANT: Saloheimo, Markku
: TITLE OF INVENTION: Microbial Swollenin Protein, DNA
: TITLE OF INVENTION: Sequences Encoding Such Swollenins and Method of Producing
: TITLE OF INVENTION: Such Swollenins
: FILE REFERENCE: GC378-2-D1
: CURRENT APPLICATION NUMBER: US/10/197,294A
: CURRENT FILING DATE: 2002-07-17
: PRIOR APPLICATION NUMBER: US 09/112,498
: PRIOR FILING DATE: 1998-07-09
: PRIOR APPLICATION NUMBER: US 08/893,766
: PRIOR FILING DATE: 1997-07-11
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6
: LENGTH: 225
: TYPE: PRT
: ORGANISM: Plant/eukaryotic
US-10-197-294A-6

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	Query Match	88.1%;	Score 1228;	DB 15;	length 225;
	Best Local Similarity	98.2%;	Pred. No. 1.2e-114;		
	Matches 223;	Conservative	1;	Mismatches 1;	Indels 2; Gaps 2;
QY	24 DYGMOSGHATFYGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSGACFEM	83			
Dh	1 DYGMOSGHATFYGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSGACFEM	60			
QY	84 TCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGWCNPPLQHEDMAEPALQIAQYRAGI	143			
Dh	61 TCTNDPKWC-PGTIRVTATNFCPPNFALPNNNGWCNPP-QHEDMAEPAFLQIAQYRAGI	118			
QY	144 VPVSFRBVPCKMKKGVRFTINGHSYFNLVLTINVGGAGDVHSYSIKSRTGWQSMRNWG	203			
Dh	119 VPVSFRBVPCKMKKGVRFTINGHSYFNLVLTINVGGAGDVHSYSIKSRTGWQSMRNWG	178			
QY	204 QNMOSNNYLNGQGSLFPVTLSDGRTLTAYNLVPSSNWQFGQTVEGPQF	250			
Dh	179 QNMOSNNYLNGQGSLFPVTLSDGRTLTAYNLVPSSNWQFGQTVEGPQF	225			

RESULT 3

US-10-197-294A-4
; Sequence 4, Application US/10197294A
; Publication No. US20030104546A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Barbara A.
; APPLICANT: Ward, Michael
; APPLICANT: Penttila, Merja

```

; APPLICANT: Pere, Jaakko
; APPLICANT: Saloheimo, Markku
; TITLE OF INVENTION: Microbial Swollenin Protein, DNA
; TITLE OF INVENTION: Sequences Encoding Such Swollenins and Method of Producing
; TITLE OF INVENTION: Such Swollenins
; FILE REFERENCE: GC378-2-D1
; CURRENT APPLICATION NUMBER: US/10/197,294A
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 09/112,498
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: US 08/893,766
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Trichoderma reesei
US-10-197-294A-4

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Query Match
Best Local

[illegible]

RESULT 4

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: Sequence 5, Application US/10197294A
: Publication No. US20030104546A1
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: GENERAL INFORMATION:
: APPLICANT: Swanson, Barbara A.
: APPLICANT: Ward, Michael
: APPLICANT: Penttila, Merja
: APPLICANT: Pere, Jaakko
: APPLICANT: Saloheimo, Markku
: TITLE OF INVENTION: Microbial Swollenin Protein, DNA
: TITLE OF INVENTION: Sequences Encoding Such Swollenins and Method of Producing
: TITLE OF INVENTION: Such Swollenins
: FILE REFERENCE: GC378-2-D1
: CURRENT APPLICATION NUMBER: US/10/197,294A
: CURRENT FILING DATE: 2002-07-17
: PRIOR APPLICATION NUMBER: US 09/112,498
: PRIOR FILING DATE: 1998-07-09
: PRIOR APPLICATION NUMBER: US 08/893,766
: PRIOR FILING DATE: 1997-07-11
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 222
:
: TYPE: PRT
: ORGANISM: Plant/eukaryotic
:
: US-10-197-294A-5

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Query Match

Query Match	79.6%;	Score 1109.5;	DB 15;	Length 222;
Best Local Similarity	88.0%;	Pred. No. 8.1e-103;		
Matches 198; Conservative	16;	Mismatches 8;	Indels 3;	Gaps 3;

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QY 26 GGMQSGHATFYGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC 85
; FILE REFERENCE: GC378-2-D1
Db 1 GGMQSAHATFYGGDASGTMGACGYGNLYSQGYGTNTALSTALFNNGLSCGACFELTC 60
; CURRENT FILING DATE: 2002-07-17
QY 86 TNDPKMCLPGTIRVTATNFCPPNFALPNNNGWCNPLQHPDMAEPALQIAQYRAGIVP 145
; PRIOR FILING DATE: 1998-07-09
Db 61 DNDPK-CLPGSITVTATNFCPPNFALPNNNGWCNPLQHPDLAQPALFKIAQYRAGIVP 119
; PRIOR APPLICATION NUMBER: US 08/893,766
QY 146 VSFRRVPCMKKGVRFTINGHSYFNLVLTITNVGAGDVHSVSIKGSRTGMQSMGRNWGN 205
; NUMBER OF SEQ ID NOS: 40
Db 120 VAYRRVPCMKRGIRFTINGHSYFNLVLTITNVGAGDVHSVSIKGSRTGMQSMGRNWGN 179
; SOFTWARE: FastSeq for windows Version 4.0
QY 206 WQNNYNGQGLSFQVTLSDGRTLTAYNLVPSPNQFGQTYEGPQF 250
; SEQ ID NO 12
Db 180 WQNSYNGQGLSFQVTLSDGRTLTAYNLVPSPNQFGQTF-GGQF 222
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Plant/eukaryotic
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(233)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-197-294A-12
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RESULT 5
US-10-150-559-4

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; Sequence 4, Application US/10150559
; Publication No. US20030221218A1
; GENERAL INFORMATION:
; APPLICANT: Wilkins, Thea A.
; TITLE OF INVENTION: The Regents of the University of California
; FILE REFERENCE: 023070-116500US
; CURRENT APPLICATION NUMBER: US/10/150,559
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Gossypium hirsutum
US-10-150-559-4
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Query Match 74.9%; Score 1044; DB 12; Length 258;
Best Local Similarity 74.3%; Pred. No. 3.4e-96;
Matches 182; Conservative 27; Mismatches 26; Indels 10; Gaps 1;

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QY 16 FFFVFTFA-----DYGMQSGHATFYGGDASGTMGACGYGNLYSQGYGTNTVA 65
; FILE REFERENCE: 023070-116500US
Db 14 FFFLFSICNSIFLGANGDDNGMQTAHATFYGADATGTMGACGYGNLYSQGYGTSTAA 73
; CURRENT FILING DATE: 2002-04-08
QY 66 LSTALFNNGLSCGACFEMTCNDPKMCLPGTIRVTATNFCPPNFALPNNNGWCNPLQHP 125
; PRIOR FILING DATE: 2002-04-08
Db 74 LSTALFNNGLSCGAFYELRCNNDPQWCISRTITVTATNFCPPNFALSSDNGWCNPPREH 133
; SOFTWARE: FastSeq for windows Version 4.0
QY 126 FDMAPALFLQIAQYRAGIVPVSFRRVPCMKKGVRFTINGHSYFNLVLTITNVGAGDVHS 185
; SEQ ID NO 9
Db 134 FDLAEPALFLQIAEYRAGIVPVSFRRVPCMKKGIRYTMNGHSYFNLVLTITNVGAGADITS 193
; LENGTH: 253
QY 186 VSIKGSRTGMQSMGRNWGNQNNYNGQGLSFQVTLSDGRTLTAYNLVPSPNQFGQTY 245
; TYPE: PRT
Db 194 VSIKGSRTGMQSMGRNWGNQNNYNGQGLSFQVTLSDGRTLTAYNLVPSPNQFGQTF 253
; ORGANISM: Zea mays
QY 246 EGPQF 250
; LENGTH: 253
Db 254 EGGQF 258
```

RESULT 6
US-10-197-294A-12

```
; Sequence 12, Application US/10197294A
; Publication No. US20030104546A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Barbara A.
; APPLICANT: Ward, Michael
; APPLICANT: Penttila, Merja
; APPLICANT: Pere, Jaako
; APPLICANT: Saloheimo, Markku
; TITLE OF INVENTION: Microbial Swollenin Protein, DNA
; TITLE OF INVENTION: Sequences Encoding Such Swollenins and Method of Producing
```

```
; TITLE OF INVENTION: Such Swollenins
; FILE REFERENCE: GC378-2-D1
; CURRENT APPLICATION NUMBER: US/10/197,294A
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 09/112,498
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: US 08/893,766
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 12
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Plant/eukaryotic
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(233)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-197-294A-12
```

Query Match 74.2%; Score 1035; DB 15; Length 233;
Best Local Similarity 78.1%; Pred. No. 2.4e-95;
Matches 178; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

```
QY 23 ADYGWQSGHATFYGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFE 82
; FILE REFERENCE: GC378-2-D1
Db 6 ADYGWQSAHATFYGGDASGTMGACGYGNLYSTGYGTNTALSTALFNDGACRSCYE 65
; CURRENT FILING DATE: 2002-07-17
QY 83 MTCNDPKMCLPGTIRVTATNFCPPNFALPNNNGWCNPLQHPDMAEPALQIAQYRAG 142
; PRIOR FILING DATE: 1998-07-09
Db 66 LRCNDGQWCLPGSITVTATNFCPPNFALPNDGWCNPPRPHDMAEPALQIGVYRAG 125
; SOFTWARE: FastSeq for windows Version 4.0
QY 143 IVPVSFRRVPCMKKGVRFTINGHSYFNLVLTITNVGAGDVHSVSIKGSRTGMQSMGRNW 202
; SEQ ID NO 9
Db 126 IVPVSYRRVPCVKKGIRFTINGHSYFNLVLTITNVAGPDVQSVSIKGSRTGMQSMGRNW 185
; LENGTH: 253
QY 203 GQNMQNNYNGQGLSFQVTLSDGRTLTAYNLVPSPNQFGQTYEGPQF 250
; TYPE: PRT
Db 186 GQNMQNSYLDGQSLSFQVAVSDGRTLTAYNLVPSPNQFGQTFEGQF 233
; ORGANISM: Zea mays
```

RESULT 7
US-10-409-701-9

```
; Sequence 9, Application US/10409701
; Publication No. US20030221224A1
; GENERAL INFORMATION:
; APPLICANT: Helentjaris, Chris
; TITLE OF INVENTION: Enhanced Silk Exsersion Under Stress
; FILE REFERENCE: 1421
; CURRENT APPLICATION NUMBER: US/10/409,701
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,796
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 9
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Zea mays
US-10-409-701-9
```

Query Match 73.7%; Score 1027; DB 12; Length 253;
Best Local Similarity 78.0%; Pred. No. 1.7e-94;
Matches 177; Conservative 25; Mismatches 25; Indels 0; Gaps 0;

```
QY 24 DYGMQSGHATFYGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEM 83
; FILE REFERENCE: GC378-2-D1
Db 27 DYGMQSAHATFYGGDASGTMGACGYGNLYSTGYGTNTALSTALFNDGACRSCYE 86
; CURRENT FILING DATE: 2002-07-17
QY 84 TCTNDPKMCLPGTIRVTATNFCPPNFALPNNNGWCNPLQHPDMAEPALQIAQYRAGI 143
; PRIOR FILING DATE: 1998-07-09
Db 87 RCDNNGQSLPGTITVTATNFCPPNFALPSDDGWCNPPRPHDMAEPALQIAQYRAGI 146
; SOFTWARE: FastSeq for windows Version 4.0
```

```
QY      144 VPVSRFRVRPCKMKGGVRFPTINGHSYFNLVLITNVGAGDVHVSISIKGRTRGQMöSRNwG 203
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      147 VPAAYRRVRVPCKKGGIRFTINGHSYFNLVLVTNVAGADEVSVSISKSSRGWQPMSRNwG 206
QY      204 QNMöSNNYLNGöGLSFöOYTLSDGRITLAYNLVPSNMöFöGTYEGPöF 250
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      207 öNMöSNSLLDGöSLSFöYTASDGRIVTSNGVAPAGWöFGöTFEGAöF 253
```

RESULT 8

```

US-09-896-301-2
; Sequence 2, Application US/09896301
; Patent No. US20020103355A1
; GENERAL INFORMATION:
; APPLICANT: Cosgrove, Daniel J
; APPLICANT: McQueen-Mason, Simon
; APPLICANT: Gultinan, Mark J
; APPLICANT: Shcherban, Tatyana
; APPLICANT: Shi, Jun
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; FILE REFERENCE: 1194/1C114US3
; CURRENT APPLICATION NUMBER: US/09/896,301
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/092,160
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 08/440,517
; PRIOR FILING DATE: 1995-05-12
; PRIOR APPLICATION NUMBER: 08/242,090
; PRIOR FILING DATE: 1994-05-12
; PRIOR APPLICATION NUMBER: 08/060,944
; PRIOR FILING DATE: 1993-05-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: rice expansin
; NAME/KEY: UNSURE
; LOCATION: 211
; OTHER INFORMATION: Xaa is unknown or other.
US-09-896-301-2

```

[illegible]

RESULT 5

```

US-10-197-294A-8
; Sequence 8, Application US/10197294A
; Publication No. US20030104546A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Barbara A.
; APPLICANT: Ward, Michael

```

```

; APPLICANT: Penttila, Merja
; APPLICANT: Pere, Jaakko
; APPLICANT: Saloheimo, Markku
; TITLE OF INVENTION: Microbial Swollenin Protein, DNA
; TITLE OF INVENTION: Sequences Encoding Such Swollenins and Method of Producing
; TITLE OF INVENTION: Such Swollenins
; FILE REFERENCE: GC378-2-D1
; CURRENT APPLICATION NUMBER: US/10/197,294A
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 09/112,498
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: US 08/893,766
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Plant/eukaryotic
US-10-197-294A-8

```

Query Match	73.0%;	Score 1017.5;	DB 15;	Length 236;
Best Local Similarity	78.6%;	Pred. No. 1.4e-93;		
Matches 176;	Conservative 23;	Mismatches 24;	Indels 1;	Gaps 1;
QY	26	GGWQSGHATPYGGGDASGTMGACAGCYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC	85	
Db	12	GGWNAHAATPYGGGDASGTMGACAGCYGNLYSQGYGTNTALSTALFNNGLSCGACFEIRC	71	
QY	86	TNDPKMCLPGTIRVTATNFCBPNNFALPNNNGWCNPPLOHFDMAEPFLQTAQYRAGIVP	145	
Db	72	QNDGKMC-PGSIVVTATNFCBPNNALPNNAGWCNPPQGHEDLSQPVFORLAQYRAGIVP	130	
QY	146	VSFRVRPCMKGKGVFTINGHSYENLVLTITNVGAGDVHSVSIKGSRTGWSMSRNMGN	205	
Db	131	VAYRRVPCVRRGGIRFTINGHSYENLVLTITNVGAGDVHSAMVYKGSRTGQMSRNMGN	190	
QY	206	WOSNNYILNGGGLSFQVTLSDGRTLTAAYNLVPSNMWQFGQTYEGPQ	249	
Db	191	WOSNSYILNGGSLSFKVTISDQTIIVSNVANAAGWSFGQITFGAQ	234	

RESULT 10

```

Sequence 9, Application US/10197294A
Publication No. US20030104546A1
GENERAL INFORMATION:
APPLICANT: Swanson, Barbara A.
APPLICANT: Ward, Michael
APPLICANT: Penttila, Merja
APPLICANT: Pere, Jaakko
APPLICANT: Saloheimo, Markku
TITLE OF INVENTION: Microbial Swollenin Protein, DNA
TITLE OF INVENTION: Sequences Encoding Such Swollenins
TITLE OF INVENTION: Such Swollenins
FILE REFERENCE: GC378-2-D1
CURRENT APPLICATION NUMBER: US/10/197,294A
CURRENT FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 09/112,498
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: US 08/893,766
PRIOR FILING DATE: 1997-07-11
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 232
TYPE: PRT
ORGANISM: Plant/eukaryotic
US-10-197-294A-9

```

query M

Query Match	72.7%;	Score 1013.5;	DB 15;	Length 232;
Best Local Similarity	77.6%;	Pred. No. 3.4e-93;		
Matches 177;	Conservative 25;	Mismatches 25;	Indels 1;	Gaps 1;

[illegible]

RESULT 11
US-09-896-301-6
; Sequence 6, Application US/09896301
; Patent No. US20020103355A1

```

: APPLICANT: Cosgrove, Daniel J
: APPLICANT: McQueen-Mason, Simon
: APPLICANT: Gultinan, Mark J
: APPLICANT: Shcherban, Tatyana
: APPLICANT: Shi, Jun
: TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
: FILE REFERENCE: 1194/1C114US3
: CURRENT APPLICATION NUMBER: US/09/896,301
: CURRENT FILING DATE: 2001-06-29
: PRIOR APPLICATION NUMBER: 09/092,160
: PRIOR FILING DATE: 1998-06-05
: PRIOR APPLICATION NUMBER: 08/440,517
: PRIOR FILING DATE: 1995-05-12
: PRIOR APPLICATION NUMBER: 08/242,090
: PRIOR FILING DATE: 1994-05-12
: PRIOR APPLICATION NUMBER: 08/060,944
: PRIOR FILING DATE: 1993-05-12
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: Patentln Ver. 2.1
: SEQ ID NO 6
:
: LENGTH: 226
:
: TYPE: PRT
: ORGANISM: Artificial Sequence
:
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis
:
: OTHER INFORMATION: expansin
:
: US-09-896-301-6

```

Query Match	72.6%;	Score 1011.5;	DB 10;	Length 226;
Best Local Similarity	77.1%;	Pred. No. 5.2e-93;		
Matches 175; Conservative	23;	Mismatches 28;	Indels 1;	Gaps 1;

[illegible]

RESULT 12

```

US-09-896-301-5
; Sequence 5, Application US/09896301
; Patent No. US20020103355A1
; GENERAL INFORMATION:
; APPLICANT: Cosgrove, Daniel J
; APPLICANT: McQueen-Mason, Simon
; APPLICANT: Gulltinan, Mark J
; APPLICANT: Shcherban, Tatyana
; APPLICANT: Shi, Jun
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; FILE REFERENCE: 1194/1C114US3
; CURRENT APPLICATION NUMBER: US/09/896,301
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/092,160
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 08/440,517
; PRIOR FILING DATE: 1995-05-12
; PRIOR APPLICATION NUMBER: 08/242,090
; PRIOR FILING DATE: 1994-05-12
; PRIOR APPLICATION NUMBER: 08/060,944
; PRIOR FILING DATE: 1993-05-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis
US-09-896-301-5

```

Query Match	69.0%;	Score 962;	DB 10;	Length 225;
Best Local Similarity	75.0%;	Pred. No. 4.6e-88;		
Matches 171; Conservative	26;	Mismatches 27;	Indels 4;	Gaps 2;

[illegible]

```

RESULT 13
US-10-197-294A-11
; Sequence 11, Application US/10197294A
; Publication No. US20030104546A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Barbara A.
; APPLICANT: Ward, Michael
; APPLICANT: Penttila, Merja
; APPLICANT: Pere, Jaakko
; APPLICANT: Saloheimo, Markku
; TITLE OF INVENTION: Microbial Swollenin Protein, DNA
; TITLE OF INVENTION: Sequences Encoding Such Swollenins and Method of Producing
; TITLE OF INVENTION: Such Swollenins
; FILE REFERENCE: GC378-2-D1
; CURRENT APPLICATION NUMBER: US/10/197,294A
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 09/112,498
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: US 08/893,766
; PRIOR FILING DATE: 1997-07-11

```

```
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Plant/eukaryotic
US-10-197-294A-11
```

```
Query Match          67.4%; Score 940; DB 15; Length 241;
Best Local Similarity 71.4%; Pred. No. 7.8e-86;
Matches 162; Conservative 28; Mismatches 35; Indels 2; Gaps 1;
```

```
QY 26 GWMQSGHATFYGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSGACFEMTC 85
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 13 GGETAHATFYGGSDASGTMGACGYGNLYSQGYVTALSTALFNNGFSGACFELKC 72

QY 86 TNDPKWCLPG--TIRVTATNFCPPNFALPNNNGWCNPPLQHFDMABPAFLQIAQYRAGI 143
    :|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 73 ASDPKWCHSGSPSIFVTATNFCPPNFAPSDNGWCNPRPHFDLAMPFELKIAEYRAGI 132

QY 144 VPVSFRVRVPCMKKGVRFTINGHSYFNVLITNVGAGDVHSVSIKSGRTGQMSRHWG 203
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 133 VPVSFRVRVPCMKKGIRFTINGFRYFNVLITNVAGAGNIVRLGVKGTHTSMWTMSRWG 192

QY 204 QNWQSNYYLNGQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPQF 250
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 193 QNWQSNVYLVGQSLSFVYTSDDRSTSWNIAPANWKFGQTFMGKNF 239
```

RESULT 14

```
US-10-197-294A-14
; Sequence 14, Application US/10197294A
; Publication No. US20030104546A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Barbara A.
; APPLICANT: Ward, Michael
; APPLICANT: Penttila, Merja
; APPLICANT: Saloheimo, Markku
; TITLE OF INVENTION: Microbial Swollenin Protein, DNA
; TITLE OF INVENTION: Sequences Encoding Such Swollenins and Method of Producing
; FILE REFERENCE: GC378-2-D1
; CURRENT APPLICATION NUMBER: US/10/197,294A
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 09/112,498
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: US 08/893,766
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Plant/eukaryotic
US-10-197-294A-14
```

```
Query Match          67.2%; Score 937; DB 15; Length 237;
Best Local Similarity 72.7%; Pred. No. 1.5e-85;
Matches 165; Conservative 21; Mismatches 39; Indels 2; Gaps 1;
```

```
QY 26 GWMQSGHATFYGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSGACFEMTC 85
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 9  GPWTSAHATFYGGSDASGTMGACGYGNLYSQGYVTALSTALFNNGLSGACFELKC 68

QY 86 TNDPKWCLPG--TIRVTATNFCPPNFALPNNNGWCNPPLQHFDMABPAFLQIAQYRAGI 143
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 69 DQDPRWCNPNPSILITATNFCPPNFAESDNGWCNPRPHFDLAMPFELKIAQYRAGI 128

QY 144 VPVSFRVRVPCMKKGVRFTINGHSYFNVLITNVGAGDVHSVSIKSGRTGQMSRHWG 203
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 129 VPVAYRRVPCRKAGGIRFTINGFRYFNVLITNVAGAGDIVRVSVKGTNTAMTMSRWG 188
```

```
QY 204 QNWQSNYYLNGQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPQF 250
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 189 QNWQSNVYFVGQALSFVYTSDDRSTSWNVAPPHWQFGQTFMGKNF 235
```

RESULT 15

```
US-10-197-294A-10
; Sequence 10, Application US/10197294A
; Publication No. US20030104546A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Barbara A.
; APPLICANT: Ward, Michael
; APPLICANT: Penttila, Merja
; APPLICANT: Saloheimo, Markku
; TITLE OF INVENTION: Microbial Swollenin Protein, DNA
; TITLE OF INVENTION: Sequences Encoding Such Swollenins and Method of Producing
; FILE REFERENCE: GC378-2-D1
; CURRENT APPLICATION NUMBER: US/10/197,294A
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 09/112,498
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: US 08/893,766
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Plant/eukaryotic
US-10-197-294A-10
```

```
Query Match          63.8%; Score 889.5; DB 15; Length 233;
Best Local Similarity 69.5%; Pred. No. 8.4e-81;
Matches 157; Conservative 26; Mismatches 34; Indels 9; Gaps 2;
```

```
QY 26 GWMQSGHATFYGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGLSGACFEMTC 85
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 14 GPWTAHATFYGGSDASGTMGACGYGNLYSQGYLTALSTALFDQGLSGACFELMC 73

QY 86 TNDPKWCLPG--TIRVTATNFCPPNFALPNNNGWCNPPLQHFDMABPAFLQIAQYRAGI 144
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 74 VNDPQWCIKGRSIVTATNFCPP-----GGACDPNNHFDLSQPIYEKIALYSGI 125

QY 145 PVVSFRVRVPCMKKGVRFTINGHSYFNVLITNVGAGDVHSVSIKSGRTGQMSRHWG 204
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 126 PVMYRRVRCKRSGGIRFTINGHSYFNVLITNVGAGDVHSVSMKSGRTKQMLMSRWG 185

QY 205 NWQSNYYLNGQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPQF 250
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 186 NWQSNYYLNGQSLSFVYTSDDRSTSWNVAPPTWSFGQTYTGQF 231
```

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Search completed: December 18, 2003, 17:55:20
Job time : 32 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2003, 22:33:47 ; Search time 2802 Seconds
(without alignments)
3650.038 Million cell updates/sec

Title: US-09-383-579C-10
Perfect score: 1394
Sequence: 1 MAFSPSPSSSLFLLPFFVF.....AYNLVPSNMQFGQTEGPQF 250

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 segs, 20454813386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09383579/runat_18122003_171927_28772/app_query.fasta_1.391
-DB=GenEmbl -QFMT=fastap -SUFFIX=xge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09383579 @CGN 1 1 4958 @runat_18122003_171927_28772 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_inv:*
4: gb_in:*
5: gb_om:*
6: gb_ov:*
7: gb_pat:*
8: gb_ph:*
9: gb_pl:*
10: gb_pr:*
11: gb_ro:*
12: gb_sts:*
13: gb_sy:*
14: gb_un:*
15: gb_vi:*
16: em_ba:*
17: em_fun:*
18: em_hum:*
19: em_in:*
20: em_mu:*
21: em_om:*
22: em_or:*
23: em_ov:*
24: em_pat:*
25: em_ph:*
26: em_pl:*
27: em_ro:*
28: em_sts:*
29: em_un:*

29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pin:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1394	100.0	992	8 CSU30382	U30382 Cucumis sat
2	1275	91.5	681	6 AR076514	AR076514 Sequence
3	1275	91.5	681	6 AR161478	AR161478 Sequence
4	1275	91.5	681	6 AX306492	AX306492 Sequence
5	1275	91.5	684	6 AX306490	AX306490 Sequence
6	1160.5	83.2	1109	8 PAU93167	U93167 Prunus arne
7	1152.5	82.7	1035	8 CAR291817	AJ291817 Cicer ari
8	1151.5	82.6	1048	8 AF297521	AF297521 Prunus ce
9	1151.5	82.6	1109	8 AF350937	AF350937 Prunus ce
10	1143.5	82.0	1088	8 AF230332	AF230332 Zinnia el
11	1141	81.9	1180	8 AB104443	AB104443 Vitis lab
12	1140	81.8	1243	8 AB093028	AB093028 Pyrus com
13	1138	81.6	1195	8 AB104444	AB104444 Vitis lab
14	1137.5	81.6	1153	8 AB093029	AB093029 Pyrus com
15	1133.5	81.3	1118	8 AB093030	AB093030 Pyrus com
16	1130.5	81.1	1142	8 AF428174	AF428174 Rumex pal
17	1125	80.7	1147	8 AF096776	AF096776 Lycopersi
18	1120	80.3	1108	8 AY083166	AY083166 Malus x d
19	1118	80.2	1177	8 AF049354	AF049354 Nicotiana
20	1117.5	80.2	1170	8 AF159563	AF159563 Fragaria
21	1116.5	80.1	1173	8 AF167360	AF167360 Rumex pal
22	1113.5	79.9	1233	8 AF350936	AF350936 Prunus ce
23	1113	79.8	1262	8 AY079206	AY079206 Mirabilis
24	1112	79.8	1070	8 AY079208	AY079208 Mirabilis
25	1111	79.7	1220	8 AB029083	AB029083 Prunus pe
26	1108	79.5	1117	8 AF428175	AF428175 Rumex pal
27	1105	79.3	1252	8 AF038815	AF038815 Prunus ar
28	1102.5	79.1	1098	8 AY083168	AY083168 Musa acum
29	1101.5	79.0	998	8 AF085330	AF085330 Pinus tae
30	1100	78.9	1175	8 AB104445	AB104445 Vitis lab
31	1092	78.3	919	8 PTU64891	U64891 Pinus taeda
32	1092	78.3	1169	8 AY299692	AY299692 Sambucus
33	1087	78.0	923	8 PTU64890	U64890 Pinus taeda
34	1085	77.8	762	6 AX506393	AX506393 Sequence
35	1085	77.8	762	6 AX651951	AX651951 Sequence
36	1085	77.8	891	8 PTU64893	U64893 Pinus taeda
37	1085	77.8	1016	8 AY086770	AY086770 Arabidops
38	1077	77.3	923	8 PTU64892	U64892 Pinus taeda
39	1076.5	77.2	1191	8 AY079205	AY079205 Mirabilis
40	1071.5	76.9	1144	6 AX392019	AX392019 Sequence
41	1063	76.3	1497	8 CAR489608	AJ489608 Cicer ari
42	1055	75.7	1245	8 AB104442	AB104442 Vitis lab
43	1054.5	75.6	1340	8 AB093031	AB093031 Pyrus com
44	1054	75.6	1355	8 AB093032	AB093032 Pyrus com
45	1053	75.5	1419	8 AF448467	AF448467 Prunus ce

RESULT 1

ALIGNMENTS

CSU30382 992 bp mRNA linear PLN 04-DEC-1996
LOCUS CSU30382
DEFINITION Cucumis sativus expansin (Cs-EXPI) mRNA, complete cds.
ACCESSION U30382
VERSION U30382.1 GI:1040874
KEYWORDS
SOURCE Cucumis sativus (cucumber)
ORGANISM Cucumis sativus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
REFERENCE
AUTHORS 1 (bases 1 to 992)
Shcherban,T.Y., Shi,J., Durachko,D.M., Guiltinan,M.J.,
McQueen-Mason,S.J., Shieh,M. and Cosgrove,D.J.
Molecular cloning and sequence analysis of expansins--a highly
conserved, multigene family of proteins that mediate cell wall
extension in plants
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 92 (20), 9245-9249 (1995)
MEDLINE 96016146
PUBMED 7568110
REFERENCE
AUTHORS 2 (bases 1 to 992)
Shcherban,T., Shi,J., Durachko,D.M., Guiltinan,M.J.,
McQueen-Mason,S.J., Shieh,M. and Cosgrove,D.J.
Direct Submission
JOURNAL Submitted (27-JUN-1995) Daniel J. Cosgrove, Biology, Pennsylvania
State University, 208 Mueller Laboratory, University Park, PA
16802, USA
FEATURES
source location/Qualifiers
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/mol_type="mRNA"
/strain="Burpee Pickler"
/db_xref="taxon:3659"
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/gene="Cs-EXPI"
154..906
/gene="Cs-EXPI"
/note="similar to pollen allergen Lol pI, Lolium perenne,
Swiss-Prot Accession Number P14946; former gene name
CuExs1; expansin-29 (Ex29) protein"
/codon_start=1
/product="expansin S1 precursor"
/protein_id="AAB37746.1"
/db_xref="GI:1040875"
/translation="MAFSYSPSSFLPFFVFTFADYGMQSGHATFYGGDASGT
MGACGYGNLYSQYGTNTVALSTALFNGLSCGACFEMTCTNDPKWCLPGTIRVTAT
NECPNFPALPNNGGWCNPLQHFDMAPAFIQAQYRAGIVPSFRVPCKMKGVR
FTINGHSYFNLVLTITNVGAGDVHSVSIKSGRTGQSMGRNWQNMQNNYLNQGLS
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223..903
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223..903
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/product="expansin S1"
/function="induces extension (creep) in plant cell walls"
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polyA_site
/gene="Cs-EXPI"
/note="17 A nucleotides"
BASE COUNT 259 a 277 c 177 g 279 t
ORIGIN
Alignment Scores:
Pred. No.: 6.23e-127 Length: 992
Score: 1394.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-09-383-579C-10 (1-250) x CSU30382 (1-992)
QY 1 MetAlaPheSerTyrSerProPheSerSerLeuPheLeuProPhePheValPhe 20
Db 154 ATGGCTTTTCTTACTACACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 213

QY 21 ThrPheAlaAspTyrGlyGlyTyrPGLnserGlyHisAlaThrPheTyrGlyGlyAsp 40
Db 214 ACCTTCGCTGACTACGGTGGCTGGCAGAGCGGCCACGCCACTTTTATGTGTGTGAC 273
QY 41 AlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGly 60
Db 274 GATCTGGACCATGGGTGAGCTTGTGGGTATGGGAATTTATACACCAAGGATATGGC 333
QY 61 ThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCys 80
Db 334 ACGAACACGGTGGCGCTGAGCACTGCGCTATTATTAACAATGATTAAGTTGTGTCTGC 393
QY 81 PheGluMetThrCysThrAsnAspProLysTyrPGLnserProGlyThrIleArgValThr 100
Db 394 TTCGAATGACTTGTACAAACGACCTTAATGTGTCTTCCGGGAACCTATTAGGGTCACT 453
QY 101 AlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnGlyGlyTyrPGLnser 120
Db 454 GCCACCAACTTTGCCCTCTCACTTGTCTCTCCCTAACACCAATGTGTGATGTGCAAC 513
QY 121 ProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArg 140
Db 514 CTTCCCTCTCCAACTTGCACATGCTGAGCTGCTTCCCTTCAAAATCGCTCAATACGA 573
QY 141 AlaGlyIleValProValSerPheArgArgValProCysMetLysGlyGlyValArg 160
Db 574 GCTGTATCGTCCCGCTCTCTCTTGTAGGTACCATGTATGAGAAAGGTGAGTGAGG 633
QY 161 PheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyAla 180
Db 634 TTTAACAATCAATGGCCACTCACTCAATCTTCAACCTGTTTGTATCAAAACGTGGTGCGCA 693
QY 181 GlyAspValHisSerValSerIleLeuGlySerArgThrGlyTyrPGLnserMetSerArg 200
Db 694 GCGCAGCTCCACTCTGTGTGATAAAGGGTCTGAACTGATGGAATCCATGCTAGA 753
QY 201 AsnTyrPGLnAsnTyrPGLnserAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGln 220
Db 754 AATTGGGGCCAAACTGGCAAGCAACAACATCAATGAGCCAAAGCCTTTCTTTCAA 813
QY 221 ValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTyrPGLn 240
Db 814 GTCACTCTTAGTATGTGTGCGCACTCTCACTGCTTAATCTCGTTCCTTCCAATGGCAA 873
QY 241 PheGlyGlnThrTyrGlyGlyProGlnPhe 250
Db 874 TTGGCCAAACCTATGAAGGCCCTCAATTG 903
RESULT 2
AR076514 681 bp DNA linear PAT 30-AUG-2000
LOCUS AR076514
DEFINITION Sequence 1 from patent US 5959082.
ACCESSION AR076514
VERSION AR076514.1 GI:10003260
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 681)
Cosgrove,D.J., McQueen-Mason,S., Guiltinan,M., Shcherban,T. and
Shi,J.
Proteins catalyzing the extension of plant cell walls
JOURNAL Patent: US 5959082-A 1 28-SEP-1999;
FEATURES location/Qualifiers
source 1..681
/organism="unknown"
BASE COUNT 161 a 179 c 164 g 177 t
ORIGIN
Alignment Scores:
Pred. No.: 1.71e-115 Length: 681
Score: 1275.00 Matches: 227
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 91.46% Indels: 0
 DB: 6 Gaps: 0

US-09-383-579C-10 (1-250) x AR076514 (1-681)

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QY 24 AsPTyrglygLYTrpGlnSerGlyHisAlaThrPheTyrglygLYAspAlaSerGly 43
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    1 GACTACGGTGGCTGGCAGAGCGGCCACGCCACCTTTATGTGTGTGTCGACGATCTGGC 60

QY 44 ThrMetGlygLYAlaCySGlyTYrGlyAsnLeuTYrSerGlnGlyTYrGlyThrAsnThr 63
    |||||
    61 ACCATGGGTGAGCTTGTGGGTATGGGAATTATACAGCCAGGGTATGGCAGACACG 120

QY 64 ValAlaLeuSerThrAlaLeuPheAsnGlyLeuSerCysGlyAlaCySPheGluMet 83
    |||||
    121 GTGGCGCTGAGCAGCTGCGCTATTAAACATGATTAAGTGTGTGCTTGTGGAATG 180

QY 84 ThrCysThrAsnAspProlySTrpCysLeuProGlyThrIleArgValThrAlaThrAsn 103
    |||||
    181 ACTGTACAAACGACCCCTAAATGATGTCCTCCGGAACTATTAGGGTCACTGCCACCAAC 240

QY 104 PheCysProProAsnPheAlaLeuProAsnAsnGlyGlyTYrPCysAsnProProLeu 123
    |||||
    241 TTTGGCCCTCCTTAACCTTGTCTCTCCCTAACACAAATGATGATGTCACCCCTCTCTC 300

QY 124 GlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTYrArgAlaGlyIle 143
    |||||
    301 CAACACTTCGACATGCGCTGAGCCCTCTCTTCAATCGCTCAATACCGAGCTGTATC 360

QY 144 ValProValSerPheArgArgValProCysMetLysGlyGlyValArgPheThrIle 163
    |||||
    361 GTCCCCGTCCTCTTTCGTAGGGTACCATGTATGAAGAAAGGTGAGTGAAGTTTACAATC 420

QY 164 AsnGlyHisSerTYrPheAsnLeuValLeuIleThrAsnValGlyGlyAlaGlyAspVal 183
    |||||
    421 AATGCCACTCATTACTTCAACCTCGTTTGTATCACAACCGTCGCTGCGCAGCGACGTC 480

QY 184 HisSerValSerIleLysGlySerArgThrGlyTYrGlnSerMetSerArgAsnTrpGly 203
    |||||
    481 CACTCTGTGTGATAAAGGGGTCTCGAACTGGCAATCCATGTCTAGAAATTGGGGC 540

QY 204 GlnAsnTrpGlnSerAsnAsnTYrLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeu 223
    |||||
    541 CAAACTGGCAAGCAACAACTATCTCAATGGCCAGGCCCTTCTTCAAGTCACTCTT 600

QY 224 SerAspGlyArgThrLeuThrAlaTYrAsnLeuValProSerAsnTrpGlnPheGlyGln 243
    |||||
    601 AGTGATGTGCGACTCTCACTGCTTAAATCTGTTCTTCCAATTGGCAATTGGCCAA 660

QY 244 ThrTYrGluGlyProGlnPhe 250
    |||||
    661 ACCTATGAAGGCCCTCAATTC 681

Db 661 ACCTATGAAGGCCCTCAATTC 681

RESULT 3
AR161478 681 bp DNA linear PAT 17-OCT-2001
LOCUS Sequence 1 from patent US 6255466.
DEFINITION AR161478
ACCESSION AR161478
VERSION AR161478.1 GI:16227385
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 681)
AUTHORS Cosgrove,D.J., McQueen-Mason,S., Guiltinan,M., Shcherban,T. and Shi,J.
TITLE Purified plant expansion proteins and DNA encoding same
JOURNAL Patent: US 6255466-A 1 03-JUL-2001;
FEATURES
SOURCE 1. 681
Location/Qualifiers
/organism="unknown"
BASE COUNT 161 a 179 c 164 g 177 t
  
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ORIGIN

Alignment Scores:
 Pred. No.: 1.71e-115 Length: 681
 Score: 1275.00 Matches: 227
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 91.46% Indels: 0
 DB: 6 Gaps: 0

US-09-383-579C-10 (1-250) x AR161478 (1-681)

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QY 24 AsPTyrglygLYTrpGlnSerGlyHisAlaThrPheTyrglygLYAspAlaSerGly 43
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QY 44 ThrMetGlygLYAlaCySGlyTYrGlyAsnLeuTYrSerGlnGlyTYrGlyThrAsnThr 63
    |||||
    61 ACCATGGGTGAGCTTGTGGGTATGGGAATTATACAGCCAGGGTATGGCAGACACAG 120

QY 64 ValAlaLeuSerThrAlaLeuPheAsnGlyLeuSerCysGlyAlaCySPheGluMet 83
    |||||
    121 GTGGCGCTGAGCAGCTGCGCTATTAAACATGATTAAGTGTGTGCTTGTGGAATG 180

QY 84 ThrCysThrAsnAspProlySTrpCysLeuProGlyThrIleArgValThrAlaThrAsn 103
    |||||
    181 ACTGTACAAACGACCCCTAAATGATGTCCTCCGGAACTATTAGGGTCACTGCCACCAAC 240

QY 104 PheCysProProAsnPheAlaLeuProAsnAsnGlyGlyTYrPCysAsnProProLeu 123
    |||||
    241 TTTGGCCCTCCTTAACCTTGTCTCTCCCTAACACAAATGATGATGTCACCCCTCTCTC 300

QY 124 GlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTYrArgAlaGlyIle 143
    |||||
    301 CAACACTTCGACATGCGCTGAGCCCTCTCTTCAATCGCTCAATACCGAGCTGTATC 360

QY 144 ValProValSerPheArgArgValProCysMetLysGlyGlyValArgPheThrIle 163
    |||||
    361 GTCCCCGTCCTCTTTCGTAGGGTACCATGTATGAAGAAAGGTGAGTGAAGTTTACAATC 420

QY 164 AsnGlyHisSerTYrPheAsnLeuValLeuIleThrAsnValGlyGlyAlaGlyAspVal 183
    |||||
    421 AATGCCACTCATTACTTCAACCTCGTTTGTATCACAACCGTCGCTGCGCAGCGACGTC 480

QY 184 HisSerValSerIleLysGlySerArgThrGlyTYrGlnSerMetSerArgAsnTrpGly 203
    |||||
    481 CACTCTGTGTGATAAAGGGGTCTCGAACTGGCAATCCATGTCTAGAAATTGGGGC 540

QY 204 GlnAsnTrpGlnSerAsnAsnTYrLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeu 223
    |||||
    541 CAAACTGGCAAGCAACAACTATCTCAATGGCCAGGCCCTTCTTCAAGTCACTCTT 600

QY 224 SerAspGlyArgThrLeuThrAlaTYrAsnLeuValProSerAsnTrpGlnPheGlyGln 243
    |||||
    601 AGTGATGTGCGACTCTCACTGCTTAAATCTGTTCTTCCAATTGGCAATTGGCCAA 660

QY 244 ThrTYrGluGlyProGlnPhe 250
    |||||
    661 ACCTATGAAGGCCCTCAATTC 681

Db 661 ACCTATGAAGGCCCTCAATTC 681

RESULT 4
AX306492 681 bp DNA linear PAT 11-DEC-2001
LOCUS Sequence 3 from Patent WO0188163.
DEFINITION AX306492
ACCESSION AX306492
VERSION AX306492.1 GI:17645712
KEYWORDS
SOURCE Cucumis sativus (cucumber)
ORGANISM Cucumis sativus
REFERENCE 1 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
  
```


Db 301 CAACACTTCGACATGGCTGAGCTGCCTTCTTCAATCGCTCAATACCGAGCTGTATC 360
QY 144 ValProValSerPheArgArgValProCysMetLysLysGlyValArgPheThrIle 163
Db 361 GTCCCCGCTCTTCTTCTGAGGTAACATGATGAAGAAAGGTGAGTGAAGTTTACAATC 420
QY 164 AsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyValArgLysAspVal 183
Db 421 AATGGCCACTCATACTTCAACTCTGTTTGATCACAACGTCGGTGCGCAGCGACGTC 480
QY 184 HisSerValSerIleLysGlySerArgThrGlyTyrGlnSerMetSerArgAsnTyrGly 203
Db 481 CACTCTGTCTGATTAAGGGGTCTCGAACTGGATGGCAATCCATGCTAGAAATTGGGGC 540
QY 204 GlnAsnTyrGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeu 223
Db 541 CAAACTGGCAAGCAACAACATACTCAATGGCCAGGCTTTCTTCAAGTCACTCTT 600
QY 224 SerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTyrGlnPheGlyGln 243
Db 601 AGTGATGGTCGCACTCTCACTGCTATATCTGTTCTTCCCAATTGGCAATTGGCCAA 660
QY 244 ThrTyrGlnGlyProGlnPhe 250
Db 661 ACCTATGAAGGCCCTCAATTC 681
RESULT 6
PAU93167 1109 bp mRNA linear PLN 01-SEP-1998
LOCUS PAU93167
DEFINITION Prunus armeniaca expansin (PA-Exp1) mRNA, complete cds.
ACCESSION U93167
VERSION U93167.1 GI:3510537
KEYWORDS
SOURCE Prunus armeniaca (apricot)
ORGANISM Prunus armeniaca
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
REFERENCE
AUTHORS Mbeguie-A-Mbeguie,D., Gomez,R.-M. and Fils-Lycaon,B.
TITLE Molecular cloning and nucleotide sequence of expansin 1 (PA-Exp1)
from apricot fruit
JOURNAL Unpublished
REFERENCE
AUTHORS 2 (bases 1 to 1109)
TITLE Mbeguie-A-Mbeguie,D., Gomez,R.-M. and Fils-Lycaon,B.
JOURNAL Direct Submission
Submitted (12-MAR-1997) Station de Technologie des Produits
Vegetaux, INRA, Site AGROPARC, Avignon 84914 Cedex 9, France
REFERENCE
AUTHORS 3 (bases 1 to 1109)
TITLE Mbeguie-A-Mbeguie,D., Gomez,R.-M. and Fils-Lycaon,B.
JOURNAL Direct Submission
Submitted (12-DEC-1997) Station de Technologie des Produits
Vegetaux, INRA, Site AGROPARC, Avignon 84914 Cedex 9, France
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/db_xref="GI:3510538"
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GGIRFTINGSHYENLVLTINWGAGDVHVSIIKGSRTGMQPMNSNMGQNSNYNLNG
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BASE COUNT 301 a 254 c 242 g 312 t
ORIGIN
Alignment Scores:
Pred. No.: 4.92e-104 Length: 1109
Score: 1160.50 Matches: 206
Percent Similarity: 88.40% Conservative: 15
Best Local Similarity: 82.40% Mismatches: 28
Query Match: 83.25% Indels: 1
DB: 8 Gaps: 1
US-09-383-579C-10 (1-250) x PAU93167 (1-1109)
QY 2 AlapheserTyrSerProPheSer---SerLeuPheLeuLeuProPhePheValPhe 20
Db 86 GCATTGCTTTAGCTCCCTAGCCCTCTCTTCTTCTTCAATCTTCACTTCATGCT 145
QY 21 ThrPheAlaAspTyrGlyGlyTyrGlnSerGlyHisAlaThrPheTyrGlyGlyAsp 40
Db 146 GCTTTGCTGATTATGAGGCTGGAGAGCGCTCATGCCACTTTTATGATGGCGGTAT 205
QY 41 AlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGly 60
Db 206 GCCTCGGGAACCATGGGGGAGCATGTGGGTATGGAACTGTACAGCCAGGATATGA 265
QY 61 ThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCys 80
Db 266 ACCAACACTGCAGCTTTAAGCACAGCCTGTTTACAAATGCTTGAGCTGTGGCTTGT 325
QY 81 PheGluMetThrCysThrAsnAspProLysTyrCysLeuProGlyThrIleArgValThr 100
Db 326 TATGAATGAGATGCAACAATGACCCCTAGATGTGTCTGCTGAAGCATCATTTGTTACT 385
QY 101 AlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTyrCysAsn 120
Db 386 GCCACAACCTTTGGCCCACTAATTGCTCAGTCCACAGACAATGGCGCTGTGCAAT 445
QY 121 ProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArg 140
Db 446 CCTCCCTCCAGACCTTGATTGGCTGAGCCTGCTTCTTCAATTTGCCAATACCGC 505
QY 141 AlaGlyIleValProValSerPheArgArgValProCysMetLysLysGlyValArg 160
Db 506 GCTGGGATTTGCTCTGTTAACCCTTCAAGAAGTGGCCCTGTATGAAGAAGGAGGAATCAGA 565
QY 161 PheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyGlyAla 180
Db 566 TTCACCATCAATGGCCACTCTTCACTTCAACCTGTTTGATCACCAACGTGGGTGCA 625
QY 181 GlyAspValHisSerValSerIleLysGlySerArgThrGlyTyrGlnSerMetSerArg 200
Db 626 GGAGACGTCACCTCAGTTTCAATCAAGGGGTCCAGAACAGGGTGGCAACCCATGTCAAGA 685
QY 201 AsnTyrGlyGlnAsnTyrGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGln 220
Db 686 AACTGGGGGCAAACTGGCAGAGCAACAATTACCTCAATGGCCAGAGCCTCTCTTCCAA 745
QY 221 ValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTyrGln 240
Db 746 GTGACCACCAAGTGACGGAAGAACTGTTACAAGCTACACGTGGCCCTGTATTTGGCAG 805
QY 241 PheGlyGlnThrTyrGlnGlyProGlnPhe 250
Db 806 TTGTGACAGCTTTCTCAGGGGTCAATTT 835
RESULT 7
CAR291817 1035 bp mRNA linear PLN 19-DEC-2000
LOCUS CAR291817
DEFINITION Cicer arietinum mRNA for expansin, clone CanExp-2.

ACCESSION AJ291817
VERSION AJ291817.1 GI:11932091
KEYWORDS expansin.
SOURCE Cicer arietinum (chickpea)
ORGANISM Cicer arietinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Ciceraceae;
Cicer.
REFERENCE 1
AUTHORS Dopico, B., Sanchez, M.A. and Labrador, E.
TITLE An second expansin is expressed in chickpea epicotyls
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1035)
AUTHORS Labrador, E.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-2000) Labrador E., Dpto. Fisiologia Vegetal,
Univ. Salamanca, Campus Miguel de Unamuno. Pza. Doctores de la
Reina s/n, E-37007, SPAIN
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Query Match: 82.68% Indels: 7
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QY 83 MetThrCysThrAsnAspProLysTyrCysLeuProGlyThrIleArgValThrAlaThr 102
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QY 123 LeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGly 142
Db 426 TTGCAACATTGATGATAGCTGAACCTGCCCTTCCTCAAAATGCTGAATATAGGCTGA 485
QY 143 IleValProValSerPheArgArgValProCysMetLysLysGlyGlyValArgPheThr 162
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QY 163 IleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyGlyAlaGlyAsp 182
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Db 786 CAACATTTCAAGAGACTCAATTT 809

RESULT 8
AF297521

LOCUS AF297521 1048 bp mRNA linear PLN 17-SEP-2000
DEFINITION Prunus avium expansin 1 (Exp1) mRNA, complete cds.
ACCESSION AF297521
VERSION AF297521.1 GI:10180016

KEYWORDS
SOURCE

ORGANISM

Prunus avium (sweet cherry)

Prunus avium
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.

1 (bases 1 to 1048)

Wu, Z. and Wierema, P.A.

Differential Expression of Expansin Genes Isolated from Sweet
Cherry (Prunus avium L.) During Fruit Ripening

Unpublished

2 (bases 1 to 1048)

Wu, Z. and Wierema, P.A.

Direct Submission

Submitted (18-AUG-2000) Agriculture and Agri-Food Canada, Pacific
Agri-Food Research Centre, 4200 Highway 97, Summerland, British

Columbia V0H 1Z0, Canada

Location/Qualifiers

FEATURES

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gene

CDS

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Db 153 GCTTTGCTGATATGTTGGTGGGAAGCGGCTCATGCCACTTTTATGTTGGGTGAT 212
QY 41 AlaSerGlyThrMetGlyglYalaCysGlyTyrglyGlnLeuTyrsSerGlnGlyTyrgly 60
Db 213 GCCTCGGAACAATGGGGGAGCATGTGGTATGGGAACCTGTATCAGCCAGGGGTATGA 272
QY 61 ThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCys 80
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QY 81 PheGluMetThrCysThrAsnAspProLysTrpCysLeuProGlyThrIleArgValThr 100
Db 333 TATGAATGAGATGCAACAATGACCCCTAGATGTTGCTGCTCGAAGCATCATTTGTTACT 392
QY 101 AlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnGlyglYtrpCysAsn 120
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Db 813 TTGTCAGACTTCTCAGGGGTCAATTT 842
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LOCUS Prunus cerasus expansin (EXP2) mRNA, complete cds.
DEFINITION
ACCESSION AF350937
VERSION AF350937.1 GI:13898650
KEYWORDS

SOURCE Prunus cerasus
ORGANISM Prunus cerasus
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QY 41 AlaSerGlyThrMetGlyglYalaCysGlyTyrglyGlnLeuTyrsSerGlnGlyTyrgly 60
Db 207 GCCTCGGAACAATGGGGGAGCATGTGGTATGGAACTTGTACAGCCAGGGGTATGA 266
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Db 267 ACCAACACTGCAGCTTAAAGCACAGCCTGTTTAAACAATGGCTTGAGCTGTGCTTGT 326
QY 81 PheGluMetThrCysThrAsnAspProLysTrpCysLeuProGlyThrIleArgValThr 100
Db 327 TATGAATGAGATGCAACAATGACCCCTAGATGTTGCTGCTGGAAGCATCATTTGTTACT 386
QY 101 AlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyglYtrpCysAsn 120
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QY 121 ProProleuGlnHisPheaspMetAlaGluProAlaPheleuGlnIleAlaGlnTyrArg 140
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QY 221 ValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTyrGln 240
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ACCESSION AF230332
VERSION AF230332.1 GI:7025492
KEYWORDS
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ORGANISM Zinnia elegans
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; Campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Zinnia.
REFERENCE 1 (bases 1 to 1088)
AUTHORS Im,K.H., Cosgrove,D.J. and Jones,A.M.
TITLE Subcellular localization of expansin mRNA in xylem cells
JOURNAL Plant Physiol. 123 (2), 463-470 (2000)
MEDLINE 20317189
PUBMED 10859177
REFERENCE 2 (bases 1 to 1088)
AUTHORS Im,K.H., Cosgrove,D.J. and Jones,A.M.
TITLE Direct Submission
JOURNAL Submitted (02-FEB-2000) Biology, University of North Carolina,
Chapel Hill, NC 27599, USA
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QY 61 ThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCys 80
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QY 81 PheGluMetThrCysThrAsnAspProLysTyrCysLeuProGlyThrIleArgValThr 100
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VERSION AB104443.1 GI:29421119
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SOURCE Vitis labrusca x Vitis vinifera
ORGANISM Vitis labrusca x Vitis vinifera
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; Vitaceae; Vitis.

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REFERENCE
1
AUTHORS Ishimaru, M. and Kobayashi, S.
TITLE Exoression of Expansin genes is related grape berry softening
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1180)
AUTHORS Ishimaru, M.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2003) Megumi Ishimaru, Osaka Prefecture
University, Graduate School of Agriculture and Biological Sciences;
1-1, Gakuen-cho, Sakai, Osaka 599-8531, Japan
(E-mail: m.ishima@plant.osakafu-u.ac.jp, Tel: 81-72-254-9419,
Fax: 81-72-254-9418)
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Alignment Scores:
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Best Local Similarity: 79.53% Mismatches: 28
Query Match: 81.85% Indels: 4
DB: 8 Gaps: 1
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Db 96 TGCCTCCAGGACACAATATGTAATGATGATGGGTGGAGAGGTGGGCATGCCAATTCTAT 155
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Db 756 GCTGCTGTGCAGTTTGGGCAACATATGAGGGGCTCAGTTT 797
RESULT 12
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LOCUS AB093028
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ACCESSION AB093028
VERSION AB093028.1 GI:29467498
KEYWORDS
SOURCE
ORGANISM
Pyrus communis (pear)
Pyrus communis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Pyrus.
1
Hiwasa, K., Rose, J.K., Nakano, R., Inaba, A. and Kubo, Y.
TITLE Differential expression of seven alpha-expansin genes during growth
and ripening of pear fruit
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1243)
AUTHORS Hiwasa, K., Kubo, Y., Nakano, R. and Inaba, A.
TITLE Direct Submission
JOURNAL Submitted (08-OCT-2002) Kyoto Hiwasa, Okayama University, Graduate
School of Natural Science and Technology, Tsushima-naka 1-1-1,
Okayama, Okayama 700-8530, Japan
(E-mail: k-hiwasa@cc.okayama-u.ac.jp, Tel: 81-86-251-8338,
Fax: 81-86-251-8338)
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BASE COUNT      377 a      261 c      293 g      312 t
ORIGIN
Alignment Scores:
Pred. No.:       5.73e-102      Length:      1243
Score:           1140.00        Matches:      210
Percent Similarity: 87.94%      Conservative: 16
Best Local Similarity: 81.71%   Mismatches:   21
Query Match:     81.78%         Indels:       10
DB:              8              Gaps:          4

US-09-383-579C-10 (1-250) x AB093028 (1-1243)
QY      1 MetAlaPheSerTYrSerProPheSerSerLeuPheLeuProPhePheValPhe 20
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Db      40 ATGGCTTTTACTCTTTCT--CACTCCACCATGCTCTTCTG-----TTCTTGCTCTC 90
QY      21 -----ThrPheAlaAspTYr---GlyGlyTTPGlnSerGlyHisAla 33
      |||||:::|||||:::|||||:::|||||:::|||||
Db      91 AATATATGCTCTTCAAGGTACTTTGGTGACTATGAGGTGAGTGGAAAGTGCCATGCC 150
QY      34 ThrPheTYrGlyGlyGlyAspAlaSerGlyThrMetGlyGlyAlaCysGlyTYrGlyAsn 53
      |||||:::|||||:::|||||:::|||||:::|||||
Db      151 ACATTATTATGTTGGTGTGATGCTTCTTGACCAATGGAGGTGCTTGATATGAAAC 210
QY      54 LeuTYrSerGlnGlyTYrGlyTYrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsn 73
      |||||:::|||||:::|||||:::|||||:::|||||
Db      211 TTGTATAGTCAAGGGTACGGAACCAACACTGCAGCACTGACACAGACTCTTCAACGAT 270
QY      74 GlyLeuSerCysGlyAlaCysPheGluMetThrCysThrAsnAspProLysTYrCysLeu 93
      |||||:::|||||:::|||||:::|||||:::|||||
Db      271 GGCTTGAGCTGCGGGTCGTATTATGATGAATGATGATGACCCCAATGTCCTC 330
QY      94 ProGlyThrIleArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsn 113
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Db      331 CCGGCAAGCATCATCGTCACCGCCACCACTTCTGCCCTCTTAACCTTGCTCAGTCCAAC 390
QY      114 AsnAsnGlyGlyTYrCysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPhe 133
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Db      391 GACATGTGTGCTGTGCAATCTCTCTCCAGCACTTCGATTTGGTGAGCCTGCTTTC 450
QY      134 LeuGlnIleAlaGlnTYrArgAlaGlyIleValProValSerPheArgArgValProCys 153
      |||||:::|||||:::|||||:::|||||:::|||||
Db      451 GAGAAATCGCTCAGTACCGAGCTGGAATGTCCCGCTCTCTTCAAGAGGTTTCATGT 510
QY      154 MetIleLysGlyGlyValArgPheThrIleAsnGlyHisSerTYrPheAsnLeuValLeu 173
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Db      511 GTGAAGAAGGAGAGTAAGATTCAACATCAACGCCCACTCATACTTCAACTTGTTTG 570
QY      174 IleThrAsnValGlyGlyAlaGlyAspValHisSerValSerIleLysGlySerArgThr 193
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Db      571 ATCAAAACGTGGAGAGACAGAGATGTGCACACTGCATGATCAAGGGCTCCACACACA 630
QY      194 GlyTPGlnSerMetSerArgAsnTrpGlyIleAsnTrpGlnSerAsnAsnTYrLeuAsn 213
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Db      631 GGGTGCAAGCCATGTGAGGAACGTGGGCCAGAACTGGCAGACAACTTTACTCAAC 690
QY      214 GlyGlnGlyLeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTYrAsn 233
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Db      691 GGCCAGAGCCTCTCTTCCAAAGTCACTACCAAGCGAGCAGACAACTCTCAACCAACAAT 750
QY      234 LeuValProSerAsnTrpGlnPheGlyGlnThrTYrGluGlyProGlnPhe 250
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Db      751 GTTGGCCCGGGGAAGTGGCAGTTTGGCCAGACATATGAGGGCAGTCAATTC 801
RESULT 13
AB104444      AB104444      1195 bp      mRNA      linear      PLN 01-APR-2003
LOCUS
DEFINITION Vitis labrusca x Vitis vinifera Vexp-3 mRNA for expansin, complete
cds.
```

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ACCESSION      AB104444
VERSION        AB104444.1 GI:29421121
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS      Ishimaru,M. and Kobayahi,S.
TITLE        Exoression of Expansin genes is related grape berry softening
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 1195)
AUTHORS      Ishimaru,M.
TITLE        Direct Submision
JOURNAL      Submitted (21-FEB-2003) Megumi Ishimaru, Osaka Prefecture
              University, Graduate School of Agriculture and Biological Sciences;
              1-1, Gakuen-cho, Sakai, Osaka 599-8531, Japan
              (E-mail:m.ishima@plant.osakafu-u.ac.jp, Tel:81-72-254-9419,
              Fax:81-72-254-9418)
FEATURES
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    1..1195
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    IRTFINGHSYFNLVLTINVAGADYRAVSIKSKTGQPMRSRMWGQMWQNSYLANGQT
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BASE COUNT    306 a      284 c      306 g      299 t
ORIGIN
Alignment Scores:
Pred. No.:       8.56e-102      Length:      1195
Score:           1138.00        Matches:      201
Percent Similarity: 87.01%      Conservative: 20
Best Local Similarity: 79.13%   Mismatches:   29
Query Match:     81.64%         Indels:       4
DB:              8              Gaps:          1

US-09-383-579C-10 (1-250) x AB104444 (1-1195)
QY      1 MetAlaPheSerTYrSerProPheSerSerLeuPheLeuProPhePheValPhe 20
      |||||:::|||||:::|||||:::|||||:::|||||
Db      49 CTCTCAATGGCTACTGACGACATTTCTTATCTCTCTTGCCCTCTTCTCTTGCTTA 108
QY      21 ThrPhe-----AlaAspTYrGlyGlyTYrGlnSerGlyHisAlaThrPheTYr 36
      |||||:::|||||:::|||||:::|||||:::|||||
Db      109 TGCCTCCAGGCGCAATGTGACTATGTGGGTGGAGGCGCGCATGCCACATTTCTAT 168
QY      37 GlyGlyGlyAspAlaSerGlyThrMetGlyGlyAlaCysGlyTYrGlyAsnLeuTYrSer 56
      |||||:::|||||:::|||||:::|||||:::|||||
Db      169 GGGGTGTGACCGCTCAGGCACAATGGGTGGGCTTGTGGGTATGGCAACTGTATACAGC 228
QY      57 GlnGlyTYrGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnGlyLeuSer 76
      |||||:::|||||:::|||||:::|||||:::|||||
Db      229 CAAGGTATGGAGCAACACTGACGCTCTCAGACCGCTCTTCAACAGTGGCTGAGC 288
QY      77 CysGlyAlaCysPheGluMetThrCysThrAsnAspProLysTYrCysLeuProGlyThr 96
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Db	289	TGTGGGGCATGTTCACGAGATGAATGCCAACGATGACCCCAATGTGTGCTCCACGGGACC	348
QY	97	IleArgValThrAlaThrAsnPheCysProProAsnPhelAlaLeuProAsnAsnAngly	116
Db	349	CTAACCGTGACTGCCACAAACTCTGCCCTCTTAACCTTGCGCTTGTCCAACCAACGCGC	408
QY	117	GlyTyrCysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIle	136
Db	409	GGATGGTGCATTCGCCCCCTTCACACCTTCGATCTAGCTGAGCCTGCCTTCCTTCAGATT	468
QY	137	AlaGlnTyrArgAlaGlyIleValProValSerPheArgArgValProCysMetIlys	156
Db	469	GCCCACTACCGAGCTGGATCGTACTGTGTCTTTCAGAAAGATGCCCTGTGTGAAGAAA	528
QY	157	GlyGlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsn	176
Db	529	GGAGGGATCCGCTTTACCATCAACGCGCCACTCCTTAACCTTGGTGTCTCATCACAAAC	588
QY	177	ValGlyGlyAlaGlyAspValHisSerValSerIleIysGlySerArgThrGlyTyrGln	196
Db	589	GTCGCCGGAGCAGACGACGTCAAGCACGATATCAATAAAGGGGCTTAAGACCGGGTGGCAG	648
QY	197	SerMetSerArgAsnTyrGlyGlnAsnTyrGlnSerAsnAsnTyrLeuAsnGlyGlnGly	216
Db	649	CCCATGTCAAGGAATGGGGCCAGAACTGGCAGAGCAACTCATTAACCTCAACGGCCAGACC	708
QY	217	LeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValPro	236
Db	709	CTCTCATTTCCAAGTCAACGAAAGCATGGCCCGGACCATGACAAAGCCTCAATGTGGCGCT	768
QY	237	SerAsnTyrGlnPheGlyGlnThrTyrGluGlyProGlnPhe	250
Db	769	GCTGGCTGGCAGTTTGGGCAACATATGAGGGGGCTCAGTTTC	810

LOCUS	AB093029	1153 bp	mRNA	linear	PLN 02-APR-2003
DEFINITION	Pyrus communis PcdExp2 mRNA for expansin, complete cds.				
ACCESSION	AB093029				
VERSION	AB093029.1	GI:29467500			
KEYWORDS					
SOURCE	Pyrus communis (pear)				
ORGANISM	Pyrus communis				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Pyrus.				
AUTHORS	1 Hiwasa, K., Rose, J.K., Nakano, R., Inaba, A. and Kubo, Y.				
TITLE	Differential expression of seven alpha-expansin genes during growth and ripening of pear fruit				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1153)				
AUTHORS	Hiwasa, K., Kubo, Y., Nakano, R. and Inaba, A.				
TITLE	Direct Submision				
JOURNAL	Submitted (08-OCT-2002) Kyoto Hiwasa, Okayama University, Graduate School of Natural Science and Technology; Tsushima-naka 1-1-1, Okayama, Okayama 700-8530, Japan				
	(E-mail: k-hiwsa@cc.okayama-u.ac.jp, Tel: 81-86-251-8338, Fax: 81-86-251-8338)				

FEATURES	Location/Qualifiers
source	1. .1153

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Score:          1137.50
Percent Similarity: 88.93%
Best Local Similarity: 81.42%
Query Match:    81.60%
DB:             8
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US-09-383-579C-10 (1-250) x AB093029 (1-1153)

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US-09-383-579C-10 (1-250) x AB093029 (1-1153)

QY      1 MetAlaPhe--SerTyrSerProPheSerLeu--PheLeuLeuProPhePhe 18
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Db      59 ATGGCTTTACTTCTCACTCCACCATTGCTCTTCTGTTCTTGTCTCAATCTATGCTT 118
QY      19 ValPheThrPheAlaAspTyr--GlyGlyTyrGlnSerGlyHisAlaThrPheTyrGly 37
      |||||  |||||  |||||  ::::|  ::::|  ::::|
Db      119 CAAGGTACTTTTGGTGACTATGAGGTGATGGAGGGCGGCCCATGTCACATTATGTT 178
QY      38 GlyGlyAspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGln 57
      |||||  |||||  |||||  |||||  |||||  |||||
Db      179 GGTGGTGATGCTCTCTGGCACAAATGGGAGGTGCTTGTGATATGGAACTTGACAGCCAA 238
QY      58 GlyTyrGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCys 77
      |||||  |||||  |||||  |||||  |||||  |||||
Db      239 GGGTACGGAAACCAACACTGCAGCACTGAGCACAGCTCTCTTCAACAATGGCTTGAGCTGC 298
QY      78 GlyAlaCysPheGluMetThrCysThrAsnAspProLysTrpCysLeuProGlyThrIle 97
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Db      299 GGGTCTTGCTATGATGAAATGTGGCAGTGAACCCCAATGTGCTCCCGGAGCAGCATC 358
QY      98 ArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGly 117
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QY      118 TrpCysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAla 137
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Db      419 TGGTGCAACCCCTCTCTCCAGCACTTGATTGGCTGAGCCTGCTTCTTGAATAATGCC 478
QY      138 GlnTyrArgAlaGlyIleValProValSerPheArgArgValProCysMetLysLysGly 157
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QY      178 GlyGlyAlaGlyAspValHisSerValSerIleLysGlySerArgThrGlyTrpGlnSer 197
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QY      198 MetSerArgAsnTrpGlyGlnAsnTrpGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeu 217
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Db      659 CTGTCAAGAAATGGGGCCAGAACTGGCAGAGCACTTACCTCAACGGCCAGAGCCTC 718
QY      218 SerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSer 237
      |||||  |||||  |||||  |||||  |||||  |||||
Db      719 TCCTTCAGGTCAACCAACGAGCGGAGAACTTCACCGCCAAACAATGTTGCGCGCGGA 778
QY      238 AsnTrpGlnPheGlyGlnThrTyrGlyGlyProGlnPhe 250

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Db 779 AACTGCGAGTTCGACCAACATTTGAGGGCAGTCAATTC 817

RESULT 15

AB093030 1118 bp mRNA linear PLN 02-APR-2003

LOCUS

DEFINITION Pyrus communis PExp3 mRNA for expansin, complete cds.

AB093030

AB093030.1 GI:29467502

KEYWORDS

SOURCE

ORGANISM

Pyrus communis (pear)

Pyrus communis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Pyrus.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

2 (bases 1 to 1118)

Hiwasa, K., Kubo, Y., Nakano, R. and Inaba, A.

Direct Submission

Submitted (08-OCT-2002) Kyoto Hiwasa, Okayama University, Graduate School of Natural Science and Technology; Tsushima-naka 1-1-1, Okayama, Okayama 700-8530, Japan

(E-mail: k-hiwasa@cc.okayama-u.ac.jp, Tel: 81-86-251-8338, Fax: 81-86-251-8338)

FEATURES

source

location/Qualifiers

1..1118

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/country="Japan"

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BASE COUNT 309 a 253 c 240 g 316 t

ORIGIN

Alignment Scores:

Pred. No.: 2.17e-101 Length: 1118

Score: 1133.50 Matches: 201

Percent Similarity: 87.60% Conservative: 18

Best Local Similarity: 80.40% Mismatches: 30

Query Match: 81.31% Indels: 1

DB: 8 Gaps: 1

US-09-383-579C-10 (1-250) x AB093030 (1-1118)

QY 2 AlapheserTyrSerProPheSer--SerLeupheLeuLeuProPhePheValPhe 20

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QY 21 ThrPheAlaAspTyrGlyGlyTyrGlnSerGlyHisAlaThrPheTyrGlyGlyAsp 40

DB 146 GTATTGCTGTTTATGAGCTGGGAAGCGCTCATGCCACATTTTACGCTGGCGTGAT 205

QY 41 AlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGly 60

DB 206 GCTTCTGGCAACATGGAGAGCATGTGTTATGGGAATTTGTACAGCCAGGGGTATGGA 265

QY 61 ThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCys 80

DB 266 ACCAAGACTGACAGCTTTGAGCAGACATGTTTCAACAATGAGCTTAAGCTGTGGTCTGT 325

QY 81 PheGluMetThrCysThrAsnAspProLysTyrCysLeuProGlyThrIleArgValThr 100

DB 326 TATGAATAGAGATGCGAACAATGACCCGAGATGTCCTGATCCATCATCTGTAAT 385

QY 101 AlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTyrCysAsn 120

DB 386 GCTACAACTTTGCCCCCTCTACTTTGCTCAGTCCACGACATGCGGATGGCAAT 445

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DB 446 CTTCTCTCCAGCATTTGATTTGGCTGAGCCCTGCTTCTTGCAATTGCCCAATACCGT 505

QY 141 AlaGlyIleValProValSerPheArgArgValProCysMetLysGlyValArg 160

DB 506 GCTGGAATCGTGGCGGTTTCTTCAAGAAGATCTTGTGTGAAGAAAGAGATAAGA 565

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DB 686 AACTGGGGTCAAAACTGGCAGAGCACTTACTCAATGGCCCAAGCCCTCTCTCCAA 745

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QY 241 PheGlyGlnThrTyrGlyGlyProGlnPhe 250

DB 806 TTGCTCAGACATTTCTCGGGGCTCAATTT 835

Search completed: December 19, 2003, 00:28:23

Job time : 2807 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2003, 22:32:07 ; Search time 258 Seconds
(without alignments)
2615.735 Million cell updates/sec

Title: US-09-383-579C-10
Perfect score: 1394
Sequence: 1 MAFSYPSPSSLFLPPFFVF.....AYNLVPSNMWQFGQTYEGPQF 250

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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Database : N_Geneseq_19Jun03:*

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2:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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4:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
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18:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
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25:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1275	91.5	681	17	AAT13320	Cucumber expansin-C. sativus DNA enc
2	1275	91.5	681	24	ABA97162	C. sativus DNA enc
3	1275	91.5	684	24	ABA97161	Arabidopsis thalia
4	1085	77.8	762	24	ABZ13283	Arabidopsis thalia
5	1085	77.8	1015	21	AAC48712	Arabidopsis thalia
6	1085	77.8	1016	21	AAC40777	Pear expansin 2 (E
7	1071.5	76.9	1144	24	AAD32964	Arabidopsis thalia
8	1041	74.7	780	21	AAC50628	Arabidopsis thalia
9	1041	74.7	1198	21	AAC33521	Arabidopsis thalia
10	1041	74.7	1233	21	AAC50633	Arabidopsis thalia
11	1036.5	74.4	753	24	ABZ12286	Arabidopsis thalia
12	1030	73.9	687	24	ABA97164	N. tabacum DNA enc
13	1026.5	73.6	1324	21	AAC47530	Arabidopsis thalia
14	1024.5	73.5	1326	21	AAC40169	Arabidopsis thalia
15	1024	73.5	747	24	ABZ13264	Arabidopsis thalia
16	1024	73.5	1236	21	AAC40035	Arabidopsis thalia
17	1011.5	72.6	1366	21	AAC47991	Arabidopsis thalia
18	1009.5	72.4	1212	21	AAC45165	Arabidopsis thalia
19	999	71.7	1167	22	AAD03713	Tomato seed expans
20	993	71.2	774	24	ABZ12284	Arabidopsis thalia
21	993	71.2	1319	21	AAC44930	Arabidopsis thalia
22	970	69.6	1205	21	AAC33121	Arabidopsis thalia
23	965	69.2	1201	21	AAC44975	Arabidopsis thalia
24	944	67.7	824	21	AAC42473	Arabidopsis thalia
25	942	67.6	1276	24	AAD32963	Pear expansin 1 (E
26	939	67.4	774	24	ABZ13037	Arabidopsis thalia
27	939	67.4	1037	21	AAC42618	Arabidopsis thalia
28	938	67.3	893	24	ABN98723	Arabidopsis thalia
29	934	67.0	1236	21	AAC34714	Arabidopsis thalia
30	928	66.6	1213	22	AAD03711	Tomato seed expans
31	919.5	66.0	2415	17	AAT30268	Cotton fibre clone
32	919.5	66.0	2415	17	AAT13053	Cotton fibre-speci
33	919.5	66.0	2415	18	AAT70039	Cotton B12 gene an
34	889.5	63.8	1291	21	AAC50400	Arabidopsis thalia
35	889.5	63.8	1293	21	AAC37064	Arabidopsis thalia
36	870	62.4	980	21	AAC41263	Arabidopsis thalia
37	857.5	61.5	1103	22	AAD03712	Tomato seed expans
38	838.5	60.2	768	24	ABZ13241	Arabidopsis thalia
39	836.5	60.0	702	20	AAV68446	Tomato expansin le
40	831	59.6	488	21	AAZ93525	Expansin gene sequ
41	826.5	59.3	1132	21	AAC38981	Arabidopsis thalia
42	795	57.0	537	20	AAV68448	Melon expansin CMe
43	786	56.4	475	21	AAZ93526	Expansin gene sequ
44	771	55.3	695	21	AAC41531	Arabidopsis thalia
45	732	52.5	501	20	AAV68447	Strawberry expansi

ALIGNMENTS

RESULT 1
AAT13320
ID AAT13320 standard; DNA; 681 BP.
XX AAT13320;
AC
XX 25-MAR-2003 (updated)
DT 08-JUL-1996 (first entry)
DT
XX Cucurbit expansin-29 cDNA.
DE
XX Expansin-29; plant cell wall; cellulose; paper recycling; de-inking;
KW polysaccharide; cucumber; ss.
XX
XX Cucumis sativus var. Burpee Pickler.
OS
XX
PN AU9540262-A.

```

XX
PD 04-APR-1996.
XX
PF 06-DEC-1995; 95AU-0040262.
XX
PR 12-MAY-1993; 93US-0060944.
PR 12-MAY-1995; 95US-0440517.
PR 12-MAY-1994; 94AU-0068320.
XX
PA (PENN-) PENN STATE RES FOUND.
XX
PI Cosgrove DJ, McQueen-Mason S;
XX
DR WPI: 1996-201150/21.
DR P-PSDB; AAR94527.
XX
PT Expansin proteins which alter the mechanical strength of
PT poly:saccharide(s) - useful in paper mfr. and recycling
XX
PS Disclosure; Page 30; 60pp; English.
XX
CC A CDNA clone (AAT13320) codes for cucumber expansin-29 (AAR94527),
CC a member of a novel class of proteins that catalyse the extension of
CC plant cell walls and the weakening of the hydrogen bonds in pure
CC cellulose. It was obt. by PCR amplification of cucumber seedling
CC cDNA using primers based on isolated peptide fragments of the protein.
CC The gene can be expressed in bacterial or other systems for use in
CC recombinant expansin prodn. Expression of the gene in transgenic
CC plants may allow alteration of plant growth characteristics,
CC while expression in plant tissue cultures may allow improved prodn.
CC of useful chemicals.
CC (Updated on 25-MAR-2003 to correct PF field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 681 BP; 161 A; 179 C; 164 G; 177 T; 0 other;

Alignment Scores:
Pred. No.: 1.48e-125 Length: 681
Score: 1275.00 Matches: 227
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 91.46% Indels: 0
DB: 17 Gaps: 0

US-09-383-579c-10 (1-250) x AAT13320 (1-681)
QY 24 AspTYRGLYGLYTRPGInSerGlyHisAlaThrPheTYRGLYGLYAspAlaSerGly 43
DB 1 GACTACGGGTGGCTGGCAGAGCGGCCACCACTTTATGTTGTTGATGACGATCTGGC 60
QY 44 ThrMetGLYGLYAlaCyseGLYTYRGLYAsnLeuTYRSerGlnGLYTYRGLYThrAsnThr 63
DB 61 ACCATGGGTGGAGCTTGTGGTATGGAAATTATACAGCCAGGGTATGGCAGAACAG 120
QY 64 ValAlaLeuSerThrAlaLeuPheAsnAsnGLYLeuSerCyseGLYAlaCysePheGluMet 83
DB 121 GTGGCGCTGAGCACTGCGCTATTTAACAATGATTAAGTTGTGTGCTTGTGCAATG 180
QY 84 ThrCyseThrAsnAspProLYSTrPCysLeuProGLYThrIleArgValThrAlaThrAsn 103
DB 181 ACTTGTAACAACGACCTTAATGTGCTTCCGGGAACATAATTAGGGTCACTGCCACCAAC 240
QY 104 PheCyseProProAsnPheAlaLeuProAsnAsnAsnGLYTYRPCysAsnProProLeu 123
DB 241 TTTTGCCCTCCTAACTTTGCTCTCCCTTAACAACAATGTGTGATGTGCAACCTCTCTC 300
QY 124 GlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTYRArgAlaGlyIle 143
DB 301 CAACACTTCGACATGGCTGAGCCTGCTTCTTCAATTCGCTCAATACCGAGCTGGTATC 360
QY 144 ValProValSerPheArgValProCyseMetLYsGLYGLYValArgPheThrIle 163
DB 361 GTCCCGCTCTCTTTCGTAGGGGTACCATGTATGAAGAAAGGTGAGTGAAGTTTACAATC 420

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QY 164 AsnGLYHisSerTYRPhenLeuValLeuIleThrAsnValGLYGLYAlaGlyAspVal 183
DB 421 AATGCCACTCACTACTTCAACCTCGTTTGATCAACAACGTCGGCGCAGGACGTC 480
QY 184 HisSerValSerIleLYsGLYSerArgThrGLYTRPGInSerMetSerArgAsnTrpGLY 203
DB 481 CACTCTGTGTGATAAAGGGGTCTGCACTGGAATGGAATCCATGTCTAGAAATTGGGGC 540
QY 204 GlnAsnTrpGlnSerAsnAsnTYRLeuAsnGLYGLYLeuSerPheGlnValThrLeu 223
DB 541 CAAAACTGGCAAGCAACAACATCTCAATGAGCCAGCCTTCTTCAAGTCACTCTT 600
QY 224 SerAspGLYArgThrLeuThrAlaTYRAsnLeuValProSerAsnTrpGlnPheGLYln 243
DB 601 AGTGATGTGCGCACTCTCACTGCTTATATCTGCTTCCATTTGGCAATTTGGCCAA 660
QY 244 ThrTYRGLYGLYProGlnPhe 250
DB 661 ACCTATGAAGGCCCTCAATTC 681

RESULT 2
ABA97162
ID ABA97162 standard; DNA; 681 BP.
XX
AC ABA97162;
DT 19-APR-2002 (first entry)
XX
DE C. sativus DNA encoding expansin csexpla.
XX
KW Expansin; cellulose-based textile; cotton; paper recycling; csexpla;
KW paper pulp; plant tissue; papermaking; gene; cucumber; ds.
XX
OS Cucumis sativus.

Key Location/Qualifiers
FT CDS 1..681
FT /tag= a
FT /partial
FT /product= "csexpla"
FT /note= "No start or stop codon given"
XX
DE10032630-A1.
XX
PD 22-NOV-2001.
XX
PF 05-JUL-2000; 2000DE-1032630.
XX
PR 16-MAY-2000; 2000DE-1023561.
XX
PA (FARB ) BAYER AG.
PI Berendes F, Rast HG, Vogt U, Gouloudis C;
XX
DR WPI: 2002-155755/21.
DR P-PSDB; AAG80769.
XX
PT Vector encoding an expansin, useful in treatment of cellulosic
PT materials for paper recycling, providing large-scale production
XX
PS Claim 2; Page 14-16; 22pp; German.
XX
CC This invention describes a novel vector (A) comprising (i) nucleic acid
CC (I) encoding an expansin (II) and (ii) coupled sequences that allow
CC expression of (I) in microorganisms. The recombinant expansins described
CC in the invention are used in preparation, treatment and finishing of
CC cellulose-based textiles (e.g. cotton) or in recycling of paper or for
CC preparation of pulp from plant tissue, as a substitute for corrosive
CC chemicals currently used in papermaking. Recombinant methods make
CC possible large scale production of expansins possible. This sequence
CC encodes the Cucumis sativus (cucumber) extensin, csexpla, described in
CC the invention.

```

XX Sequence 681 BP, 161 A, 178 C, 164 G, 178 T, 0 other;
 SQ

Alignment Scores:

Pred. No.: 1.48e-125 Length: 681
 Score: 1275.00 Matches: 227
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 91.46% Indels: 0
 DB: 24 Gaps: 0

US-09-383-579C-10 (1-250) x ABA97162 (1-681)

OY 24 AspTyrGlyGlyTrpGlnSerGlyHisAlaThrPheTyrGlyGlyGlyAspAlaSerGly 43
 DB 1 GACTACGGTGGCTGGCAGAGCGCCACGCCACTTTATGTTGGTGGTGCATCTGGC 60
 OY 44 ThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThr 63
 DB 61 ACCATGGGTGAGCTTGTGGGTATGGGAATTATACAGCCAGGCTATGGCAGAACACG 120
 OY 64 ValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGluMet 83
 DB 121 GTGGCGCTGAGCACTGCGCTATTAAACAATGATTAAGTTGGTGGTCTTGCTCGAAATG 180
 OY 84 ThrCysThrAsnAspProlyseTrpCysLeuProGlyThrIleArgValThrAlaThrAsn 103
 DB 181 ACTTGTAACAACGATCCTAAATGGTGCTCTCCGGAACTATAGGGTCACTGCCACCAAC 240
 OY 104 PheCysProProAsnPheAlaLeuProAsnAsnAsnGlyTyrCysAsnProProLeu 123
 DB 241 TTTTGCCCTCCTAACTTGTCTCTCCCTAACACAATGGTGAATGGTCAACCTCTCTC 300
 OY 124 GlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGlyIle 143
 DB 301 CAACATTTGCATAGCTGAGCCTGCTCTTCAATCGCTCATATACGAGCCGGTATC 360
 OY 144 ValProValSerPheArgArgValProCysMetLysGlyGlyValArgPheThrIle 163
 DB 361 GTCCCCGTCTCTTCTTGTAGGGTATCATGTATGAAGAAGGTGAGTGAAGTTACAATC 420
 OY 164 AsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyGlyAlaGlyAspVal 183
 DB 421 AATGGCCACTCATCTCACTCCTGTTTGTATCACAACGTCGCTGGCGCAGCGCAGCTC 480
 OY 184 HisSerValSerIleLeuGlySerArgThrGlyTyrGlnSerMetSerArgAsnTrpGly 203
 DB 481 CACTCTGTGTGATTAAGGGGTCTCGAAGCTGCAATCCATGTCTAGAAATTGGGGC 540
 OY 204 GlnAsnTrpGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeu 223
 DB 541 CAAAACTGGCAAAACAACAACATCTCAATGGCCCAAGGCTTCTTCAAGTCACTCTT 600
 OY 224 SerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGlnPheGlyGln 243
 DB 601 AGTGATGTGGCACTCTCACTGCTATTAATCTGTTCTTCCAAATTGGCAATTGGCCAA 660
 OY 244 ThrTyrGlyGlyPProGlnPhe 250
 DB 661 ACCTATGAAGGCCCTCAATTTC 681

RESULT 3

ABA97161
 ID ABA97161 standard; DNA; 684 BP.

XX ABA97161;
 AC

XX 19-APR-2002 (first entry)
 DT

XX C. sativus DNA encoding SI expansin homologue.
 DE

XX Expansin; SI; cellulose-based textile; cotton; paper recycling;
 KW

paper pulp; plant tissue; papermaking; gene; cucumber; ds.

XX Cucumis sativus.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 1..684
 FT /*tag= a
 FT /partial
 FT /product= "SI expansin homologue"
 FT /note= "No start codon given"

DE10032630-A1.

PN 22-NOV-2001.

PD 05-JUL-2000; 2000DE-1032630.

PF 16-MAY-2000; 2000DE-1023561.

PR (FARB) BAYER AG.

PI Berendes F, Raat HG, Vogt U, Gouloudis C;

XX WPI; 2002-155755/21.

DR P-PSDB; AAG80768.

PT Vector encoding an expansin, useful in treatment of cellulosic materials for paper recycling, providing large-scale production

XX Claim 2; Page 11-14; 22pp; German.

XX This invention describes a novel vector (A) comprising (i) nucleic acid (I) encoding an expansin (II) and (ii) coupled sequences that allow expression of (I) in microorganisms. The recombinant expansins described in the invention are used in preparation, treatment and finishing of cellulose-based textiles (e.g. cotton) or in recycling of paper or for preparation of pulp from plant tissue, as a substitute for corrosive chemicals currently used in papermaking. Recombinant methods make possible large scale production of expansins possible. This sequence encodes the Cucumis sativus (cucumber) SI expansin homologue described in the invention.

SQ Sequence 684 BP, 163 A, 179 C, 164 G, 178 T, 0 other;

Alignment Scores:

Pred. No.: 1.49e-125 Length: 684
 Score: 1275.00 Matches: 227
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 91.46% Indels: 0
 DB: 24 Gaps: 0

US-09-383-579C-10 (1-250) x ABA97161 (1-684)

OY 24 AspTyrGlyGlyTyrGlnSerGlyHisAlaThrPheTyrGlyGlyGlyAspAlaSerGly 43
 DB 1 GACTACGGTGGCTGGCAGAGCGCCACGCCACTTTATGTTGGTGGTGCATCTGGC 60
 OY 44 ThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThr 63
 DB 61 ACCATGGGTGAGCTTGTGGGTATGGGAATTATACAGCCAGGCTATGGCAGAACACG 120
 OY 64 ValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGluMet 83
 DB 121 GTGGCGCTGAGCACTGCGCTATTAAACAATGATTAAGTTGGTGGTCTTGCTTGAATG 180
 OY 84 ThrCysThrAsnAspProlyseTrpCysLeuProGlyThrIleArgValThrAlaThrAsn 103
 DB 181 ACTTGTAACAACGATCCTAAATGGTGCTCTCCGGAACTATAGGGTCACTGCCACCAAC 240
 OY 104 PheCysProProAsnPheAlaLeuProAsnAsnAsnGlyTyrCysAsnProProLeu 123
 DB 241 TTTTGCCCTCCTAACTTGTCTCTCCCTAACACAATGTTGATGGTGAACCTCTCTC 300

QY 124 GlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGlyIle 143
DB 301 CAACACTTCGACATGCTGAGCCTGCTTCTTCAATCGCTCAATACCGAGCTGTATC 360
QY 144 ValProValSerPheArgValProCysMetLysGlyGlyValArgPheThrIle 163
DB 361 GTCCCGCTCTCTTCGTAGGGTACATGATGAAGAAAGGTGAGTGAAGTTACAAATC 420
QY 164 AsnGlyHisSerTyrPheAsnLeuValIleThrAsnValGlyGlyAlaGlyAspVal 183
DB 421 AATGGCCACTCATCTCAACCTCGTTTGTATCACAACGTCGGTGGCAGCGACGTC 480
QY 184 HisSerValSerIleLysGlySerArgThrGlyTyrPglInSerMetSerArgAsnTyrGly 203
DB 481 CACTCTGTGTGATGAAGGGGTCTCGAATCGATGGCAATCCATGTCTGAAGAAATGGGGC 540
QY 204 GlnAsnTyrPglInSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeu 223
DB 541 CAAAACTGGCAAGCAACAATCTCAATGCGCAAGGCTTCTTCAAGTCACTCTT 600
QY 224 SerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTyrPglInPheGlyGln 243
DB 601 AGTATGCTGCGACACTCTCACTGCTTAATCTGTTCTTCCAAATGCGCAATTTGGCCAA 660
QY 244 ThrTyrGluGlyProGlnPhe 250
DB 661 ACCTATGAAGGCCCTCAATTC 681

RESULT 4

ABZ13283 standard; DNA; 762 BP.

ABZ13283;

21-JAN-2003 (first entry)

Arabidopsis thaliana stress regulated gene SEQ ID NO 1088.

Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

Arabidopsis thaliana.

WO200216655-A2.

28-FEB-2002.

24-AUG-2001; 2001WO-US26685.

24-AUG-2000; 2000US-227866P.

26-JAN-2001; 2001US-264647P.

22-JUN-2001; 2001US-300111P.

(SGRI) SCRIPPS RES INST.

(SYGN) SYNGENTA PARTICIPATIONS AG.

Harper JF, Kreps J, Wang X, Zhu T;

WPI; 2002-304127/34.

Identifying a stress condition to which a plant cell has been exposed

and producing plants with increased tolerance to these abiotic stresses

Claim 144; SEQ ID NO 1088; 577bp + Sequence listing; English.

The invention relates to identifying a stress condition to which a plant

cell has been exposed, comprising:

(a) contacting nucleic acid representative of expressed polynucleotides

in the plant cell with an array or probes representative of the plant

cell genome; and

(b) detecting a profile of expressed polynucleotides in the plant cell

characteristic of a stress response. The method is useful in the

production of transgenic plants, cells and seeds and in producing plants

CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
CC in methods of the invention.
CC Note: The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied to Derwent by
CC the European Patent Office.

SO Sequence 762 BP; 202 A; 196 C; 184 G; 180 T; 0 other;

Alignment Scores:

Pred. No.: 2,35e-105 Length: 762

Score: 1085.00 Matches: 194

Percent Similarity: 86.75% Conservative: 22

Best Local Similarity: 77.91% Mismatches: 31

Query Match: 77.83% Indels: 2

DB: 24 Gaps: 2

US-09-383-579c-10 (1-250) x ABZ13283 (1-762)

QY 4 SerTyrSerProPheSerSerLeuPheLeuLeuProPhePheVal---PheThrPhe 22
DB 13 TCATACTTAATAATATTCATATATCTCATATATATCCGATATATCTCCCAAGAACTCAT 72
QY 23 AlaAspTyrGlyGlyTyrPglInSerGlyHisAlaThrPheTyrGlyGlyAspAlaSer 42
DB 73 GGAGACGACGAGAGGTGGCAAGGTGTACGCCACGTTTACGGCGCGGAAGATCTCC 132
QY 43 GlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsn 62
DB 133 GGCAACCATGGCGGAGCTGTGTGCTATGAAATTTGTATGGCCAGGTTACGGGACGAAC 192
QY 63 ThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGlu 82
DB 193 ACGGCGGCTTAAAGTACGCGCTATATTCACAACGCACTCACGCTGGCGCTGTATGAG 252
QY 83 MetThrCysThrAsnAspProLysTyrCysLeuProGlyThrIleArgValThrAlaThr 102
DB 253 ATGAAGTGAACGATGACCCGAGGTGTGTCTCGGCTCAACCATCACCGTACACCTACA 312
QY 103 AsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTyrCysAsnProPro 122
DB 313 AACTTTGGCCACCTAACCTGCGCTCTCCACAGATATATGAGGTTGTGCAATCTCTCT 372
QY 123 LeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGly 142
DB 373 CTTCAGCATTTGCACTCGCCGAGCCAGCTTTCTTCAGATCGCTCAGTATCGTCCGGC 432
QY 143 IleValProValSerPheArgValProCysMetLysLysGlyGlyValArgPheThr 162
DB 433 ATTGTCTCTGCTCTTCCGAAGGTATCAATGTAAGAAAGGAATTAAGTTTACG 492
QY 163 IleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyGlyAlaGlyAsp 182
DB 493 ATCAACGACACTCATCTCAACTCGTTCTGATCTCCAACGTAAGAGAGAGAGAC 552
QY 183 ValHisSerValSerIleLysGlySerArgThr---GlyTyrPglInSerMetSerArgAsn 201
DB 553 GTACACGCGCTTCAATCAAAAGGCTCAAAACACAGCTCGTGGCAAGCATGTCTTAAGAAC 612
QY 202 TrrPglInAsnTrrPglInSerAsnTyrLeuAsnGlyGlnGlyLeuSerPheGlnVal 221
DB 613 TGGGACAAAACGTGACAGCAATTCATACATGAACGACCAAGGCTTCTTCCAGGTA 672
QY 222 ThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrrPglPhe 241
DB 673 ACGACGACGATGTGCGACACTGTGTAACGACGATGCTCTTCTAATTGGCAGTTC 732
QY 242 GlyInThrTyrGluGlyProGlnPhe 250
DB 733 GGACAAACCTACCAAGGTGTGTCAGTTC 759

RESULT 5

AAC48712

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ID  AAC48712 standard; DNA; 1015 BP.
XX
AC  AAC48712;
XX
DT  18-OCT-2000 (first entry)
XX
DE  Arabidopsis thaliana DNA fragment SEQ ID NO: 58484.
XX
KW  Hybridisation assay; genetic mapping; gene expression control;
KW  protein identification; signal transduction pathway;
KW  metabolic pathway; promoter; termination sequence; ss.
XX
OS  Arabidopsis thaliana.
XX
PN  EP103405-A2.
XX
PD  06-SEP-2000.
XX
PF  25-FEB-2000; 2000EP-0301439.
XX
PR  25-FEB-1999; 99US-0121825.
PR  05-MAR-1999; 99US-0123180.
PR  09-MAR-1999; 99US-0123548.
PR  23-MAR-1999; 99US-0125788.
PR  25-MAR-1999; 99US-0126264.
PR  29-MAR-1999; 99US-0126785.
PR  01-APR-1999; 99US-0127462.
PR  06-APR-1999; 99US-0128234.
PR  08-APR-1999; 99US-0128714.
PR  16-APR-1999; 99US-0129845.
PR  19-APR-1999; 99US-0130077.
PR  21-APR-1999; 99US-0130449.
PR  23-APR-1999; 99US-0130510.
PR  28-APR-1999; 99US-0130891.
PR  30-APR-1999; 99US-0132048.
PR  30-APR-1999; 99US-0132407.
PR  04-MAY-1999; 99US-0132484.
PR  05-MAY-1999; 99US-0132485.
PR  06-MAY-1999; 99US-0132486.
PR  06-MAY-1999; 99US-0132487.
PR  07-MAY-1999; 99US-0132863.
PR  11-MAY-1999; 99US-0134256.
PR  14-MAY-1999; 99US-0134218.
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Mismatches: 31
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US-09-383-579c-10 (1-250) x AAC48712 (1-1015)

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QY 23 AlaSerTyrGlyGlyTyrPglInserGlyHisAlaThrPheTyrGlyGlyGlyAspAlaSer 42
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AC 17-OCT-2000 (first entry)

DT Arabidopsis thaliana DNA fragment SEQ ID NO: 29509.

XX Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

XX EP1033405-A2.

PD 06-SEP-2000.

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QY 222 ThrLeuSerAspGlyArgThrLeuThrAlaTYrAsnLeuValProSerAsnTYrPGLInPhe 241
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RESULT 7

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AAD32964;

01-JUL-2002 (first entry)

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Pear; cell wall hydrolase; beta-galactosidase; pectin methyl esterase;
PME; beta-Gal; polygalacturonase; PG; expansin1; Exp1; expansin2; Exp2;
fruit ripening; gene expression; transgenic plant; transgenic; enzyme;
gene; ss.

Pyrus communis.

Location/Qualifiers

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WO200216613-A2.

28-FEB-2002.

20-AUG-2001; 2001WO-PT00021.

22-AUG-2000; 2000PT-0102511.

(ICAT-) ICAT INST CIENCIA APLICADA E TECNOLOGIA.

Matias Fonseca SC, Balde A, Soares Pais MS;

WPI, 2002-280942/32.

P-PsDB; AAE20571, AAE20578.

New beta-galactosidase, pectin methyl esterase, polygalacturonase,
expansin1, and expansin2 proteins and nucleic acids, useful for
regulating fruit ripening or creating transgenic plants -
Claim 14; Page 38-39; 45pp; English.

CC The present invention relates to novel genes which encode cell wall
CC hydrolases such as beta-galactosidase (beta-Gal), pectin methylesterase
CC (PME), polygalacturonase (PG) and cell wall proteins such as expansin1
CC (Exp1) and expansin2 (Exp2) proteins from pear fruit. The nucleic acids
CC are useful for regulating fruit ripening and for suppressing endogenous
CC beta-Gal, PME, PG, Exp1 and Exp2 genes in any fruit or other plant
CC organs, thus modifying the structure of the cell walls of the fruit or
CC plant and providing for ripe yet firm fruit and vegetables. The genes
CC may be used to screen a cDNA library or a genomic library from any
CC species, to inhibit or enhance gene expression or to produce transgenic
CC plants. The present sequence is a cDNA encoding pear expansin 2 protein.
XX
SQ Sequence 1144 BP; 325 A; 258 C; 242 G; 319 T; 0 other;

Alignment Scores:

Pred. No.:	1.12e-103	Length:	1144
Score:	1071.50	Matches:	199
Percent Similarity:	86.17%	Conservative:	19
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US-09-383-579c-10 (1-250) x AAD32964 (1-1144)

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QY 41 AlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGly 60
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QY 61 ThrAsnThrValAlaLeuSerThr-AlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCy 80
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AC AAC50628;
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DT 18-OCT-2000 (first entry)
XX
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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US-09-383-579C-10 (1-250) x AAC50628 (1-780)

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QY 86 ThrAsnAspProLysTYrCysLeuProG1YThrIleArgValThrAlaThrAsnPheCys 105
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RESULT 9
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ID AAC33521 standard; DNA; 1198 BP.

XX AAC33521;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 3354.

XX Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

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PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.

PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Alignment Scores:

Pred. No.: 2.04e-100 Length: 1198
Score: 1041.00 Matches: 179
Percent Similarity: 89.78% Conservative: 23
Best Local Similarity: 79.56% Mismatches: 23
Query Match: 74.68% Indels: 0
DB: 21 Gaps: 0

US-09-383-579C-10 (1-250) x AAC33521 (1-1198)

QY 26 GlyGlyTyrGlnSerGlyHisAlaThrPheTyrGlyGlyIyaAPAlaSerGlyThrMet 45
DB 125 GGGCGTTGGATCAACGCTCACGCCACTTTTACGGTGTGTGATGCTTCCGGCACAATG 184
QY 46 GlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThrValAla 65
DB 185 GGTGTGCTTGTGGATATAGTAATCTATATAGCCAGGCTACGGGACGAGCAGCGGGCT 244
QY 66 LeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGluMetThrCys 85
DB 245 CTAGCACAGCTCTCTTCAACAATGAGCTTAGCTGTGTTCTTCTTGTGAGATAGATGT 304
QY 86 ThrAsnAspProLysTyrCysLeuProGlyThrIleArgValThrAlaThrAsnPheCys 105
DB 305 GAACAAGATGTAATGTTGTTTACCTGGCTCAATCGTTGTAACTTCAAACTTCTGC 364
QY 106 ProProAsnPheAlaLeuProAsnAsnAsnGlyTyrCysAsnProProLeuGlnHis 125
DB 365 CCGCCAAATTAACGGCTTAGCGAACATATATGGCGTTGGTGTATCTCTCTTGAACAC 424
QY 126 PheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGlyIleValPro 145
DB 425 TTTGACCTTGCTCAGCTGTTTTCAACGCATGTCTAGTACAGCTGGAATGTCCT 484
QY 146 ValSerPheArgArgValProCysMetLysLysGlyGlyValArgPheThrIleAsnGly 165
DB 485 GTTTCCTACAGAGGGTTCCTTGACAGAGAGAGGAATTAAGATTACGATTAACGGC 544
QY 166 HisSerTyrPheAsnLeuValLeuIleThrAsnValGlyIyaAlaGlyAspValHisSer 185
DB 545 CACTCATACTTCAACCTTGTGCTGATCACAAACGTGGTGTGCGGAGACGTTCACTCG 604
QY 186 ValSerIleLysGlySerArgThrGlyTyrGlnSerMetSerArgAsnTyrGlyGlnAsn 205
DB ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||


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Db      605 GCGGCGATCAAGGTTCAAGAACAGTGTGCAAGCTATGTCAAGAACTGGGGCAAAAT 664
Qy      206 TrpGlnSerAsnAsnTyrLeuAnGlyGlnGlyLeuSerPheGlnValThrLeuSerAsp 225
        |||||
Db      665 TGGCAAAAGCACTTACCTCAACGCTCAAGCACTTCCCTTAAGTCAACCAACGACGAC 724
Qy      226 GtYArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGlnPheGlyGlnThrTyr 245
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Db      725 GGGCGCACAGTGTCTCTCCTTCAACGCGCTCCTGCCGCTGGTCTTATGCGCAGACTTTT 784
Qy      246 GtUGlyProGlnPhe 250
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Db      785 GCGGTTGACAGTTC 799

RESULT 10
AAC50633
ID      AAC50633 standard; DNA; 1233 BP.
XX
AC      AAC50633;
XX
DT      18-OCT-2000 (first entry)
XX
DE      Arabidopsis thaliana DNA fragment SEQ ID NO: 65567.
XX
KW      Hybridisation assay; genetic mapping; gene expression control;
KW      protein identification; signal transduction pathway;
KW      metabolic pathway; promoter; termination sequence; ss.
XX
OS      Arabidopsis thaliana.
XX
PN      EP1033405-A2.
XX
PD      06-SEP-2000.
XX
PF      25-FEB-2000; 2000EP-0301439.
XX
PR      25-FEB-1999; 99US-0121825.
PR      05-MAR-1999; 99US-0123180.
PR      09-MAR-1999; 99US-0123548.
PR      23-MAR-1999; 99US-0125788.
PR      25-MAR-1999; 99US-0126264.
PR      29-MAR-1999; 99US-0126785.
PR      01-APR-1999; 99US-0127462.
PR      06-APR-1999; 99US-0128234.
PR      08-APR-1999; 99US-0128714.
PR      16-APR-1999; 99US-0129845.
PR      19-APR-1999; 99US-0130077.
PR      21-APR-1999; 99US-0130449.
PR      23-APR-1999; 99US-0130510.
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PR      30-APR-1999; 99US-0132407.
PR      04-MAY-1999; 99US-0132484.
PR      05-MAY-1999; 99US-0132485.
PR      06-MAY-1999; 99US-0132486.
PR      06-MAY-1999; 99US-0132487.
PR      07-MAY-1999; 99US-0132863.
PR      11-MAY-1999; 99US-0134256.
PR      14-MAY-1999; 99US-0134218.
PR      14-MAY-1999; 99US-0134219.
PR      14-MAY-1999; 99US-0134221.
PR      14-MAY-1999; 99US-0134370.
PR      18-MAY-1999; 99US-0134768.
PR      19-MAY-1999; 99US-0134941.
PR      20-MAY-1999; 99US-0135124.
PR      21-MAY-1999; 99US-0135353.
PR      24-MAY-1999; 99US-0135629.
PR      25-MAY-1999; 99US-0136021.
PR      27-MAY-1999; 99US-0136392.
PR      28-MAY-1999; 99US-0136782.
PR      01-JUN-1999; 99US-0137222.
PR      03-JUN-1999; 99US-0137528.
PR      04-JUN-1999; 99US-0137502.
PR      07-JUN-1999; 99US-0137724.
PR      08-JUN-1999; 99US-0138094.
PR      10-JUN-1999; 99US-0138540.
PR      10-JUN-1999; 99US-0138847.
PR      14-JUN-1999; 99US-0139119.
PR      16-JUN-1999; 99US-0139452.
PR      16-JUN-1999; 99US-0139453.
PR      17-JUN-1999; 99US-0139492.
PR      18-JUN-1999; 99US-0139454.
PR      18-JUN-1999; 99US-0139455.
PR      18-JUN-1999; 99US-0139456.
PR      18-JUN-1999; 99US-0139457.
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PR      18-JUN-1999; 99US-0139750.
PR      18-JUN-1999; 99US-0139763.
PR      21-JUN-1999; 99US-0139817.
PR      22-JUN-1999; 99US-0139899.
PR      23-JUN-1999; 99US-0140353.
PR      23-JUN-1999; 99US-0140354.
PR      24-JUN-1999; 99US-0140695.
PR      28-JUN-1999; 99US-0140823.
PR      29-JUN-1999; 99US-0140991.
PR      30-JUN-1999; 99US-0141287.
PR      01-JUL-1999; 99US-0141842.
PR      01-JUL-1999; 99US-0142154.
PR      02-JUL-1999; 99US-0142055.
PR      06-JUL-1999; 99US-0142390.
PR      08-JUL-1999; 99US-0142803.
PR      09-JUL-1999; 99US-0142920.
PR      12-JUL-1999; 99US-0142977.
PR      13-JUL-1999; 99US-0143542.
PR      14-JUL-1999; 99US-0143624.
PR      15-JUL-1999; 99US-0144005.
PR      16-JUL-1999; 99US-0144085.
PR      16-JUL-1999; 99US-0144086.
PR      19-JUL-1999; 99US-0144325.
PR      19-JUL-1999; 99US-0144331.
PR      19-JUL-1999; 99US-0144332.
PR      19-JUL-1999; 99US-0144333.
PR      19-JUL-1999; 99US-0144334.
PR      19-JUL-1999; 99US-0144335.
PR      20-JUL-1999; 99US-0144632.
PR      20-JUL-1999; 99US-0144632.
PR      20-JUL-1999; 99US-0144884.
PR      21-JUL-1999; 99US-0144814.
PR      21-JUL-1999; 99US-0145086.
PR      21-JUL-1999; 99US-0145088.
PR      21-JUL-1999; 99US-0145088.
PR      22-JUL-1999; 99US-0145087.
PR      22-JUL-1999; 99US-0145089.
PR      22-JUL-1999; 99US-0145192.
PR      23-JUL-1999; 99US-0145145.
PR      23-JUL-1999; 99US-0145218.
PR      23-JUL-1999; 99US-0145224.
PR      26-JUL-1999; 99US-0145276.
PR      27-JUL-1999; 99US-0145913.
PR      27-JUL-1999; 99US-0145918.
PR      27-JUL-1999; 99US-0145919.
PR      28-JUL-1999; 99US-0145951.
PR      02-AUG-1999; 99US-0146386.
PR      02-AUG-1999; 99US-0146388.
PR      03-AUG-1999; 99US-0146389.
PR      04-AUG-1999; 99US-0147204.
PR      04-AUG-1999; 99US-0147302.
PR      05-AUG-1999; 99US-0147192.
PR      05-AUG-1999; 99US-0147260.
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PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
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PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Alignment Scores:
Pred. No.: 2.13e-100

Length:

1233

Score: 1041.00 Matches: 179
Percent Similarity: 89.78% Conservative: 23
Best Local Similarity: 79.56% Mismatches: 23
Query Match: 74.68% Indels: 0
DB: 21 Gaps: 0

US-09-383-579C-10 (1-250) x AAC50633 (1-1233)

QY 26 GlyGlyTyrGlnSerGlyHisAlaThrPheTyrGlyGlyGlyAspAlaSerGlyThrMet 45
Db 163 GGCCTGTGATCAACGCTCAGCCACCTTTTACCGTGTGTGATGCTTCCGGCAATG 222
QY 46 GlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThrValAla 65
Db 223 GGTGTGCTTGTGATATGTTAATCTATATAGCCAAAGGCTACGGACGACGCGCGCT 282
QY 66 LeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGluMetThrCys 85
Db 283 CTAGCACAGCTCTCTTCAACAATGACTTAGCTGTGTTCTTCTTGAATAGATGT 342
QY 86 ThrAsnAspProIysTyrCysLeuProGlyThrIleArgValThrAlaThrAsnPheCys 105
Db 343 GAAACGATGTTAATGTTGTTTACCTGCTCAATCGTTGTAACCGCTACAACTTCTGC 402
QY 106 ProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTyrCysAsnProProLeuGlnHis 125
Db 403 CCGCCAAATTAACGCGTTAGCGAACAATATGCGGTTGTGTATCTCTCTTGAACAC 462
QY 126 PheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGlyIleValPro 145
Db 463 TTTGACCTTGTCTGACCTGTTTTCACGACATGCTCAGTACGAGCTGGAATGTCCT 522
QY 146 ValSerPheArgArgValProCysMetIysGlyGlyValArgPheThrIleAsnGly 165
Db 523 GTTTCCTACAGAGGTTCTCTTGCAGAGAGAGAGAAATAGATTACAGATTAACGCG 582
QY 166 HisSerTyrPheAsnLeuValLeuIleThrAsnValGlyGlyAlaGlyAspValHisSer 185
Db 583 CACTCATACTTCAACCTTGTGCTATCACAAACGTCGGTGTGCGGAGACGTTCACTCG 642
QY 186 ValSerIleIysGlySerArgThrGlyTyrGlnSerMetSerArgAsnTyrGlyAsn 205
Db 643 GCGGCGATCAAGGTTCAAGAACAAGTGTGCAAGCTATGTCAAGAACTGGGGCAAAAT 702
QY 206 TrrGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeuSerAsp 225
Db 703 TGGCAAGCAACTCTTCAAGCGTCAAGCACTTCTTAAAGTCAACCAACGCGAC 762
QY 226 GlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTyrGlnPheGlyGlnThrTyr 245
Db 763 GGCAGACAGTGTCTCTTCAACGCGGCTCTGCGGCTGTATGCGCAGACTTTT 822
QY 246 GluGlyProGlnPhe 250
Db 823 GCGGTTGACAGCTTC 837
RESULT 11
ABZ12286
ID ABZ12286 standard; DNA; 753 BP.
XX ABZ12286;
AC
XX
DT 21-JAN-2003 (first entry)
XX
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 91.
XX
KM Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200216655-A2.
XX
PD 28-FEB-2002.

XX 24-AUG-2001; 2001WO-US26685.
 PF
 XX 24-AUG-2000; 2000US-227866P.
 PR
 PR 26-JAN-2001; 2001US-264647P.
 PR 22-JUN-2001; 2001US-300111P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Harper JF, Kreps J, Wang X, Zhu T;
 XX
 DR WPI; 2002-304127/34.
 XX
 PT Identifying a stress condition to which a plant cell has been exposed
 PT and producing plants with increased tolerance to these abiotic stresses
 PT
 XX
 PS Claim 144; SEQ ID NO 91; 577pp + Sequence Listing; English.
 XX
 CC The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising:
 CC (a) contacting nucleic acid representative of expressed polynucleotides
 CC in the plant cell with an array or probes representative of the plant
 CC cell genome; and
 CC (b) detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
 CC in methods of the invention.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied to Derwent by
 CC the European Patent Office.
 CC
 XX
 SQ Sequence 753 BP; 196 A; 187 C; 187 G; 183 T; 0 other;

Alignment Scores:
 Pred. No.: 3.18e-100 Length: 753
 Score: 1036.50 Matches: 181
 Percent Similarity: 83.74% Conservative: 25
 Best Local Similarity: 73.58% Mismatches: 31
 Query Match: 74.35% Indels: 9
 DB: 24 Gaps: 1

US-09-383-579C-10 (1-250) x ABZ12286 (1-753)

QY 13 LeuLeuProPhePhePheValPheThrPheAlaAspTyr----- 25
 DB 7 CTTGTACACCTTCTTGTATTATGCTACCCCTTGAGACATGACGTCAATGTTAC 66
 QY 26 -----GlyGlyTyrGlnSerGlyHisAlaThrPheTyrGlyGlyGlyAspAlaSerGly 43
 DB 67 GCCGAGAGAGTGGGTCAACGACACACGACATTTACGGTGTGTGATGCTTCCGGC 126
 QY 44 ThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThr 63
 DB 127 ACAATGGAGAGTGTGTGATACGAAACTATATAGCCAAAGCTATGGAACCAACACG 186
 QY 64 ValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGluMet 83
 DB 187 GCGGCGCTAAGCAGCGCTCTATTCAATAATGCTTAAGTGTGTGCTTGCAGATA 246
 QY 84 ThrCysThrAsnAspProLysTyrCysLeuProGlyThrIleArgValThrAlaThrAsn 103
 DB 247 AGATGTCAAAACGATGGAATGTGTCTTCTGCTCAATTGCTGCACACCAACAAAC 306
 QY 104 PheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTyrCysAsnProProLeu 123
 DB 307 TTTTGCCTCTTCAACACGCTTACCGAACACGAGAGGTGTGTAACTCTCTCCTCAG 366
 QY 124 GlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGlyIle 143

DB 367 CAGCATTTGATCTCTCTCAGCCCGTATTTCACGCATCGCTCATATACAGCCGCATT 426
 QY 144 ValProValSerPheArgArgValProCysMetLysGlyGlyValArgPheThrIle 163
 DB 427 GTCCCCGCTGCTTACCGAAGAGTGCCTGCGGTGAGAAGAGAGAAATTAAGTTTACGATA 486
 QY 164 AsnGlyHisSerTyrPheAsnLeuValIleThrAsnValGlyValAlaGlyAspVal 183
 DB 487 AACGACACTCTTACTTCAACTAGTCTGATCATACTACGTCGAGAGACCGAGATGTT 546
 QY 184 HisSerValSerIleLysGlySerArgThrGlyTyrGlnSerMetSerArgAsnTyrGly 203
 DB 547 CACTCAGCATGTTAAAGGTTCAAGACTGATGCGCAAGCATGTCAAGAACTGGCGA 606
 QY 204 GlnAsnTyrGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeu 223
 DB 607 CAGAACTGGCAGAGTAAGTCTTACCTTAACGACAAATCTCTCATTCAAAGTTACACA 666
 QY 224 SerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTyrGlnPheGlyGln 243
 DB 667 AGCGATGGCCAAACCATGTCTCTAACAACGTTGCTACGACGAGCTGTCTTCCGCCAG 726
 QY 244 ThrTyrGlnGlyProGln 249
 DB 727 ACCTTCACAGGTGCGCAG 744
 RESULT 12
 ABA97164
 ID ABA97164 standard; DNA; 687 BP.
 XX
 AC ABA97164;
 XX
 DT 19-APR-2002 (first entry)
 XX
 DE N. tabacum DNA encoding expansin ntxp4a.
 XX
 KW Expansin; cellulose-based textile; cotton; paper recycling; csexp4a;
 KW paper pulp; plant tissue; papermaking; gene; tobacco; ds.
 XX
 OS Nicotiana tabacum.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 1..687
 FT /*tag= a
 FT /partial
 FT /product= "ntexp4a"
 FT /note= "No start or stop codon disclosed"
 PN DE10032630-A1.
 XX
 PD 22-NOV-2001.
 XX
 PF 05-JUL-2000; 2000DE-1032630.
 XX
 PR 16-MAY-2000; 2000DE-1023561.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Berendes F, Raet HG, Vogt U, Gouloudis C;
 XX
 DR WPI; 2002-155755/21.
 DR P-PSDB; AAG80771.
 XX
 PT Vector encoding an expansin, useful in treatment of cellulosic
 PT materials for paper recycling, providing large-scale production
 XX
 PS Claim 2; Page 19-21; 22pp; German.
 XX
 CC This invention describes a novel vector (A) comprising (i) nucleic acid
 CC (I) encoding an expansin (II) and (ii) coupled sequences that allow
 CC expression of (I) in microorganisms. The recombinant expansin described
 CC in the invention are used in preparation, treatment and finishing of
 CC cellulose-based textiles (e.g. cotton) or in recycling of paper or for

CC preparation of pulp from plant tissue, as a substitute for corrosive
 CC chemicals currently used in papermaking. Recombinant methods make
 CC possible large scale production of extensins possible. This sequence
 CC encodes the lycopersicon esculentum (tomacco) extensin, ntxp4a, described
 CC in the invention.

XX Sequence 687 BP, 183 A, 128 C, 170 G, 206 T, 0 other;

Alignment Scores:

Pred. No.:	1.36e-99	Length:	687
Score:	1030.00	Matches:	175
Percent Similarity:	88.89%	Conservative:	25
Best Local Similarity:	77.78%	Mismatches:	25
Query Match:	73.89%	Indels:	0
DB:	24	Gaps:	0

US-09-383-579c-10 (1-250) x ABA97164 (1-687)

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QY 26 G1YGLYTRPGLNserG1YH1sAlathrPheTYRGLYGLYAspAlasergLYthrMet 45
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Db 10 GGAGTTGGATTAAATGCTCATGCTACTTTATGTTGGTGTGATGCTCTGGCACAATG 69.
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QY 46 G1YGLYAlaCysGLYTYRGLYAsnLeuTYRserGLNGLYTYRGLYThrAsnThrValAla 65
    |||||
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Alignment Scores:

Pred. No.: 1.32e-98 Length: 1326
Score: 1024.50 Matches: 185
Percent Similarity: 79.78% Conservative: 28
Beat Local Similarity: 69.29% Mismatches: 35
Query Match: 73.49% Indels: 19
DB: 21 Gaps: 4

-US-09-383-579C-10 (1-250) x AAC40169 (1-1326)

Qy 3 PheSerTyrSerPro-----PheSerSer---LeuPheLeu----- 13
Db 44 TTCTCTCACTCTCCATTAAGCTCTGCACCTTCTCAAGAAGATGTTTCATGGTAAG 103
Qy 14 -----LeuProPhePhePheValPheThrPheAlaAspTyrGly 26
Db 104 ATGGGTCTTTTGGGAATGCTCTGTGTGTTTGTCTGCAATGCTGTCTGTTTCATGGA 163
Qy 27 -----GlyTyrGlnSerGlyHisAlaThrPheTyrGlyGlyAspAlaSerGly 43
Db 164 TATGACGCTGGATGGGTCAATGCTCATGCTAACCCTTCTATGTGGAAGTATGCTTCAGGA 223
Qy 44 ThrMetGlyGlyAlaCyGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThr 63
Db 224 ACAATGGTGAGCTTGTGGCTACGGGAACCTCTACAGTCAAGGTTACGGGACCAACACG 283
Qy 64 ValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCyGlyAlaCySpheGluMet 83
Db 284 GCGGCGTTGAGCAGCTGCTGTCTCAACACGCTTACGTCGGGGCGGCTTTTGAGATC 343
Qy 84 ThrCysThrAsnAspProLysTyrCysLeuProGlyThrIleArgValThrAlaThrAsn 103
Db 344 AAGTGTGAGCGAGCGGCGGTGTGTTTACCAACGCTGAGTGCAGTGCATGTCACAGCCACCAAT 403
Qy 104 PheCysProProAsnPheAlaLeuProAsnAsnGlyGlyTyrCysAsnProProLeu 123
Db 404 TTCTGTCTCTTACACAGCCTCTTCCCAATAACGCTGTGTGTGTGTGTGTGTGTGTGTGT 463
Qy 124 GlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGlyIle 143
Db 464 CATCATTTGATCTCTCTCAGCCCTGTTTTCACGCAATGCTCAGTACAAAGCTGTGTGT 523
Qy 144 ValProValSerPheArgArgValProCysMetLysLysGlyGlyValArgPheThrIle 163
Db 524 GTCCCTGTTTCTTACAGAGGGTTCGCTGTATGAGAGAGGAGGTATAGATTTCACAATC 583

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QY 164 AsnGlyHisSerTyrPheAsnLeuValleuIleThrAsnValGlyGlyAlaGlyAspVal 183
Db 584 AACGGTCACTCTTACTTCAACCTTGCTTGTGACCAATGTTGGTGTGAGATGTT 643
QY 184 HisSerValSerIleLeuGlySerArgThrGlyTyrGlnSerMetSerArgAsnTyrGly 203
Db 644 CATTGGTTCGGTTAAAGTTCTAGACAAGGTGGCAACAATGTCAAGAACTGGGGA 703
QY 204 GlnAsnTyrGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeu 223
Db 704 CAGAACTGGCAAGACACAATCTCTTAAACGGTCAAGCATTTGATTTAAGTGACTGCT 763
QY 224 SerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTyrGlnPheGlyGln 243
Db 764 AGTGATGTCGTACCGTCTCTTAACACATTGCTCAGCTAGTTGCTCTTGACAA 823
QY 244 ThrTyrGlnGlyProGlnPhe 250
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RESULT 15
ABZ13264
ID ABZ13264 standard; DNA; 747 BP.
XX AC ABZ13264;
XX DT 21-JAN-2003 (first entry)
XX DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1069.
XX KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX OS Arabidopsis thaliana.
XX PN WO200216655-A2.
XX PD 28-FEB-2002.
XX PF 24-AUG-2001; 2001WO-US26685.
XX PR 24-AUG-2000; 2000US-227866P.
XX PR 26-JAN-2001; 2001US-264647P.
XX PR 22-JUN-2001; 2001US-300111P.
XX PA (SCRI ) SCRIPPS RES INST.
XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX PI Harper JF, Kreps J, Wang X, Zhu T;
XX DR WPI; 2002-304127/34.
XX PT Identifying a stress condition to which a plant cell has been exposed
XX PT and producing plants with increased tolerance to these abiotic stresses
XX PS Claim 144; SEQ ID NO 1069; 577bp + Sequence listing; English.
XX XX The invention relates to identifying a stress condition to which a plant
XX CC cell has been exposed, comprising:
XX CC (a) contacting nucleic acid representative of expressed polynucleotides
XX CC in the plant cell with an array or probes representative of the plant
XX CC cell genome; and
XX CC (b) detecting a profile of expressed polynucleotides in the plant cell
XX CC characteristic of a stress response. The method is useful in the
XX CC production of transgenic plants, cells and seeds and in producing plants
XX CC with increased tolerance to abiotic stress. The present sequence is that
XX CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
XX CC in methods of the invention.
XX CC Note: The sequence data for this patent is not represented in the printed
XX CC specification but is based on sequence information supplied to Derwent by
XX CC the European Patent Office.
SQ Sequence 747 BP; 166 A; 169 C; 192 G; 220 T; 0 other;

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Alignment Scores:
Pred. No.: 6.63e-99 Length: 747
Score: 1024.00 Matches: 175
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Best Local Similarity: 78.12% Mismatches: 26
Query Match: 73.46% Indels: 0
DB: 24 Gaps: 0

US-09-383-579C-10 (1-250) x ABZ13264 (1-747)
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QY 47 GlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThrValAlaLeu 66
Db 130 GGAGCTGTGGCTACGGGAACCTCTACAGTTACGGGACCAACACGGCGGCTTG 189
QY 67 SerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGlnMetThrCysThr 86
Db 190 AGCACTGCTCTGTCAACAACGGTCTTAGCTCGCGGCTGTTTGAGATCAAGTGTACG 249
QY 87 AsnAspProLysTyrPcysLeuProGlyThrIleArgValThrAlaThrAsnPheCysPro 106
Db 250 AGCGACGGCGCGGTGTGTTTACCTGCTGCTATCATGTGCACAGCCACCAATTTCTGCT 309
QY 107 ProAsnPheAlaLeuProAsnAsnAsnGlyGlyTyrPcysAsnProProLeuGlnHisPhe 126
Db 310 CCTAACACAGCTCTTCCCAATAACGCTGCTGTTGTTGTTAACCCTCCGCTTCATCATTC 369
QY 127 AspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGlyIleValProVal 146
Db 370 GATCTCTCAGCCTGTTTTCACAGCATTCGTCAGTACAAAGCTGTGTCTCCTGTT 429
QY 147 SerPheArgArgValProCysMetLysLysGlyGlyValArgPheThrIleAsnGlyHis 166
Db 430 TCCTACAGAGGGTTCCTGCTATGAGAAGAGGATTAAGATTCAATCAACGGTCAC 489
QY 167 SerTyrPheAsnLeuValleuIleThrAsnValGlyGlyAlaGlyAspValHisSerVal 186
Db 490 TCTTACTTCAACCTTGTCTTGTGACCAATGTGTGTGTGCTGAGATGTTCAATTCGGTT 549
QY 187 SerIleLysGlySerArgThrGlyTyrGlnSerMetSerArgAsnTyrGlyGlnAsnTyr 206
Db 550 GCGGTTAAAGTTCTTAGACACAGGTGGCAACAATGTCAAGAACTGGGACAGACTGG 609
QY 207 GlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeuSerAspGly 226
Db 610 CAAAGCAACAATCTTAAACGGTCAAGCATTTGATTTAAGGTGACTGCTAGTATGCT 669
QY 227 ArgThrLeuThrAlaTyrAsnLeuValProSerAsnTyrGlnPheGlyGlnThrTyrGlu 246
Db 670 CGTACCGTGTCTTAAACAACATTGCTCAGCTAGTTGTTGCTTTGGACAAACCTTCACC 729
QY 247 GlyProGlnPhe 250
Db 730 GGCGGTCAATTTC 741

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Search completed: December 18, 2003, 23:41:27
Job time : 263 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2003, 23:29:07 ; Search time 78 Seconds
(without alignments)
1414.690 Million cell updates/sec

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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Issued Patents_NA:*

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- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1275	91.5	681	2	US-08-440-517A-1 Sequence 1, Appl1
2	1275	91.5	681	3	US-09-092-160-1 Sequence 1, Appl1
3	919.5	66.0	2415	1	US-07-885-970A-26 Sequence 26, Appl1
4	919.5	66.0	2415	1	US-08-298-687A-26 Sequence 26, Appl1
5	919.5	66.0	2415	1	US-08-298-829-26 Sequence 26, Appl1
6	841.5	60.4	702	4	US-09-362-642-1 Sequence 1, Appl1
7	839.5	60.2	702	2	US-08-845-539-1 Sequence 1, Appl1
8	797	57.2	537	2	US-08-845-539-5 Sequence 5, Appl1
9	797	57.2	537	4	US-09-362-642-5 Sequence 5, Appl1
10	732	52.5	501	2	US-08-845-539-3 Sequence 3, Appl1
11	732	52.5	501	4	US-09-362-642-3 Sequence 3, Appl1
12	706	50.6	727	1	US-07-885-970A-6 Sequence 6, Appl1

13	706	50.6	727	1	US-08-298-687A-6	Sequence 6, Appl1
14	706	50.6	727	1	US-08-530-797-5	Sequence 5, Appl1
15	706	50.6	727	1	US-08-298-829-6	Sequence 6, Appl1
16	706	50.6	727	2	US-08-787-335-5	Sequence 5, Appl1
17	324.5	23.3	279	4	US-09-313-294A-1276	Sequence 1276, Ap
18	249.5	17.9	1072	1	US-07-971-096-1	Sequence 1, Appl1
19	249.5	17.9	1072	1	US-08-175-096-1	Sequence 1, Appl1
20	236	16.9	759	3	US-08-441-507-20	Sequence 20, Appl
21	236	16.9	759	4	US-07-969-875A-20	Sequence 5, Appl1
22	233	16.7	810	3	US-08-413-974-5	Sequence 5, Appl1
23	233	16.7	810	3	US-08-434-418-5	Sequence 5, Appl1
24	233	16.7	810	3	US-08-433-288-5	Sequence 5, Appl1
25	233	16.7	810	3	US-08-174-739A-5	Sequence 5, Appl1
26	233	16.7	810	4	US-08-434-256-5	Sequence 5, Appl1
27	233	16.7	1123	1	US-07-971-096-3	Sequence 3, Appl1
28	233	16.7	1123	1	US-08-175-096-3	Sequence 3, Appl1
29	173	12.4	775	3	US-08-441-507-3	Sequence 3, Appl1
30	173	12.4	775	4	US-07-969-875A-3	Sequence 3, Appl1
31	173	12.4	802	3	US-08-441-507-18	Sequence 18, Appl
32	173	12.4	802	4	US-07-969-875A-18	Sequence 18, Appl
33	173	12.4	832	3	US-08-441-507-19	Sequence 19, Appl
34	173	12.4	832	4	US-07-969-875A-19	Sequence 19, Appl
35	150.5	10.8	1645	4	US-09-112-498A-1	Sequence 1, Appl1
36	145	10.4	2614	4	US-09-004-056-1	Sequence 1, Appl1
37	142.5	10.2	368	3	US-08-441-507-22	Sequence 22, Appl
38	142.5	10.2	368	4	US-07-969-875A-22	Sequence 22, Appl
39	119.5	8.6	756	3	US-08-413-974-3	Sequence 3, Appl1
40	119.5	8.6	756	3	US-08-434-418-3	Sequence 3, Appl1
41	119.5	8.6	756	3	US-08-433-288-3	Sequence 3, Appl1
42	119.5	8.6	756	3	US-08-174-739A-3	Sequence 3, Appl1
43	119.5	8.6	756	4	US-08-434-256-3	Sequence 3, Appl1
44	103.5	7.4	4403765	3	US-09-103-840A-2	Sequence 2, Appl1
45	103.5	7.4	4411529	3	US-09-103-840A-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-440-517A-1
; Sequence 1, Application US/08440517A
; Patent No. 5959082
; GENERAL INFORMATION:
; APPLICANT: COSGROVE, DANIEL J.;
; APPLICANT: GUILTINAN, MARK;
; APPLICANT: SCHERBAN, TATYANA;
; APPLICANT: SHI, JUN
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
; ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,517A
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 681
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
; US-08-440-517A-1

Alignment Scores:

Pred. No.:	9.54e-137	Length:	681
Score:	1275.00	Matches:	227
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	91.46%	Indels:	0
DB:	2	Gaps:	0

US-09-383-579C-10 (1-250) x US-08-440-517A-1 (1-681)

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QY      24  AsPTyrgIyGIyTrpGInserGIyHIsAlaThrPheTyrgIyGIyAlaSPAlaSerGIy  43
Db      1  GACTACGGTGGCTGGCAGAGCGGCCACCCCTTTATAGTGTGTGACGCACTGGC  60

QY      44  ThrMetGIyGIyAlaCySGIyTyrgIyAsnLeuTySerGIyngIyTyrgIyThrAsnThr  63
Db      61  ACCATGGGTGAGCTGTGGTATGGGAATTATACAGCCAAGGTAATGGCAGCAACG  120

QY      64  ValAlaLeuSerThrAlaLeuPheAsnAsnGIyLeuSerCySGIyAlaCySPheGIyMet  83
Db      121  GTGGCGCTGAGCACTGCGCTATTAAACAATGATTAAGTTGTGTGCTTGCCTTGAATG  180

QY      84  ThrCySThrAsnAspProLySTrpCySLeuProGIyThrIleArgValThrAlaThrAsn  103
Db      181  ACTTGTAACAACGACCCCTAAATGATGTCCTCCGGGAACCTATTAGGTCACCTGCCAAC  240

QY      104  PheCySProProAsnPheAlaLeuProAsnAsnAsnGIyGIyTrpCySAsnProProLeu  123
Db      241  TTTTGCCCTCTTAACCTTGCTCTCCCAACAACAATGGTGGATGGTGAACCTCTCTC  300

QY      124  GlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrrArgAlaGIyIle  143
Db      301  CAACACTTCGACATGGCTGAGCCTGCTTCTCAATCGCTCAATACCGAGCTGTATC  360

QY      144  ValProValSerPheArgArgValProCySMetIySGIyGIyValArgPheThrIle  163
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QY      164  AsnGIyHisSerTyrrPheAsnLeuValIleThrAsnValGIyGIyAlaGIyAspVal  183
Db      421  AATGCCACTCATCTCAACCTCGTTTGATCACAACGTCGTGGGCAAGCGAGTC  480

QY      184  HisSerValSerIleIySGIySerArgThrGIyTrpGInserMetSerArgAsnTrpGIy  203
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QY      204  GlnAsnTrpGlnSerAsnAsnTyrrLeuAsnGIyGlnIyLeuSerPheGlnValThrLeu  223
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QY      224  SerAspGIyArgThrLeuThrAlaTyrrAsnLeuValProSerAsnTrpGlnPheGIyGln  243
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RESULT 2

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US-09-092-160-1
; Sequence 1, Application US/09092160C
; Patent No. 6255466
; GENERAL INFORMATION:
; APPLICANT: Cosgrove, Daniel J
; APPLICANT: McQueen-Mason, Simon
; APPLICANT: Guilfinan, Mark J
; APPLICANT: Shcherban, Tatyana
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; FILE REFERENCE: 1194/1C114US3
; CURRENT APPLICATION NUMBER: US/09/092,160C
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 08/440,517

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; EARLIER FILING DATE: 1995-05-12
; EARLIER APPLICATION NUMBER: 08/242,090
; EARLIER FILING DATE: 1994-05-12
; EARLIER APPLICATION NUMBER: 08/060,944
; EARLIER FILING DATE: 1993-05-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA cucumber
; OTHER INFORMATION: expansin
US-09-092-160-1

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Alignment Scores:

Pred. No.:	9.54e-137	Length:	681
Score:	1275.00	Matches:	227
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	91.46%	Indels:	0
DB:	3	Gaps:	0

US-09-383-579C-10 (1-250) x US-09-092-160-1 (1-681)

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QY      24  AsPTyrgIyGIyTrpGInserGIyHIsAlaThrPheTyrgIyGIyAlaSPAlaSerGIy  43
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QY      44  ThrMetGIyGIyAlaCySGIyTyrgIyAsnLeuTySerGIyngIyTyrgIyThrAsnThr  63
Db      61  ACCATGGGTGAGCTGTGGTATGGGAATTATACAGCCAAGGTAATGGCAGCAACAG  120

QY      64  ValAlaLeuSerThrAlaLeuPheAsnAsnGIyLeuSerCySGIyAlaCySPheGIyMet  83
Db      121  GTGGCGCTGAGCACTGCGCTATTAAACAATGATTAAGTTGTGTGCTTGCCTTGAATG  180

QY      84  ThrCySThrAsnAspProLySTrpCySLeuProGIyThrIleArgValThrAlaThrAsn  103
Db      181  ACTTGTAACAACGACCCCTAAATGATGTCCTCCGGGAACCTATTAGGTCACCTGCCAAC  240

QY      104  PheCySProProAsnPheAlaLeuProAsnAsnAsnGIyGIyTrpCySAsnProProLeu  123
Db      241  TTTTGCCCTCTTAACCTTGCTCTCCCAACAACAATGGTGGATGGTGAACCTCTCTC  300

QY      124  GlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrrArgAlaGIyIle  143
Db      301  CAACACTTCGACATGGCTGAGCCTGCTTCTTCAATCGCTCAATACCGAGCTGTATC  360

QY      144  ValProValSerPheArgArgValProCySMetIySGIyGIyValArgPheThrIle  163
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QY      164  AsnGIyHisSerTyrrPheAsnLeuValIleThrAsnValGIyGIyAlaGIyAspVal  183
Db      421  AATGCCACTCATCTCAACCTCGTTTGATCACAACGTCGTGGGCGCAGCGAGTC  480

QY      184  HisSerValSerIleIySGIySerArgThrGIyTrpGInserMetSerArgAsnTrpGIy  203
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Db      601  AGTGATGTGCGCACTCTCACTGCCATTAATCTCGTTCTTCCAATTGGCAATTGGCCAA  660

QY      244  ThrTyrgIuGIyProGlnPhe  250
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; APPLICATION NUMBER: US/08/298,687A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/617,239
; FILING DATE: 21-NOV-1990
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/253,243
; FILING DATE: 04-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 283-2478
; TELEFAX: (608) 251-5139
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2415 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Gossypium barbadense
; STRAIN: Sea Island
; IMMEDIATE SOURCE:
; LIBRARY: EMBL-SI
; CLONE: SIB12
; US-08-298-687A-26

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Alignment Scores:

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Query Match: 65.96% Indels: 56
DB: 1 Gaps: 2

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US-09-383-579C-10 (1-250) x US-08-298-687A-26 (1-2415)

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QY 3 PheSerTyrSerProPheSerSerLeuPheLeuProPhePheValPheThrPhe 22
   |||:::|||||:::|||||:::|||||
Db 784 TTTCACCTTTCTCTTGTGTGTCAGTGTATGCACTCCATTTCCTTGCTGCTAATGCA- 842

QY 23 AlaAspTyrGlyGlyTyrPglInSerGlyHisAlaThrPheTyrGlyGlyAspAlaSer 42
   |||:::|||||:::|||||:::|||||
Db 843 GATGACATGTGTGTTG-CAAACTGCCATGC-ACCTTCTACGGTGTGCTGATGCTACC 900

QY 43 GlyThrMet----- 45
   |||:::|||||
Db 901 GGCACATGGGTGAGTTCAACTTTCAAACCATTAACCTACATAAAATCTTAGGCTAT 960

QY 46 -----GlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerG1 57
   |||:::|||||:::|||||
Db 961 GTTCTTAATTGTGATGTTTCTATAGGGGAGCTTGCTGTTATGAAACCTGTACAGTCA 1020

QY 57 nglyTyrGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCy 77
   |||:::|||||:::|||||
Db 1021 AGGSTATGGAACGACACAGCAGCTTTGAGCACTGCACTTTTCAACATGGCTTGAGCTG 1080

QY 77 sglyAla-CysPheGluMetThrCysThrAsnAspProlySTyrCysLeuProGlyThri 97
   |||:::|||||:::|||||
Db 1081 CGGTGCACTGCTACGAGCTCCGGTGCACAATGATCTCAATGTGTGCTTAGTCAACCA 1140

QY 97 leArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyG 117
   |||:::|||||:::|||||
Db 1141 TAACCGTGACAGCCACCACTTTTGTGCCCCCTAATGCTTATCTAGTGACAAATGGCG 1200

QY 117 lyTyrCysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIlea 137
   |||:::|||||:::|||||
Db 1201 GGtGTGCAATCCCCCAGACGAAACACTTTGATTGGCCGAACCGGCACTTCTTGACATCG 1260

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QY 137 lagIntYrArgAlaGlyIleValProValSerPheArg----- 149
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Db 1261 CGGATATCGAGCTGGAATCGTCCCTGTATGTTCAGAGGTGGTGAATAAACTCAATT 1320

QY 150 -----ArgVal 151
   |||:::|||||
Db 1321 CAATCATCACACTCTTAAAGTATGTAAACTGTGGGTGTTAACTTTTGACGGGTG 1380

QY 152 ProCysMetIleValGlyGlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeu 171
   |||:::|||||:::|||||
Db 1381 TCATGTGTGAAGAAAGAGGCAATCAGGTACACCATGAATGACATTGCTACTTCAACATG 1440

QY 172 ValLeuIleThrAsnValGlyGlyAlaGlyAspValHisSerValSerIleGlySer 191
   |||:::|||||:::|||||
Db 1441 GTGTGTGTAACCAACGTTGGAGGGGAGGAGATATAACGTCAAGTGTCCATCAAGTCTCC 1500

QY 192 ArgThrGlyTyrPglInSerMetSerArgAsnTyrPglInAsnTyrPglInSerAsnAsnTyr 211
   |||:::|||||:::|||||
Db 1501 AAACAGATGGCTAACCCTATGTCTCAGAAATTGGGGCCAAACTGGCAGCAATGCTTAC 1560

QY 212 LeuAsnGlyGlnGlyLeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAla 231
   |||:::|||||:::|||||
Db 1561 CTTAACGGCCCAAGCCTCTCTTCAAGTACTGCCAGCATGCGACACTATCAACAAC 1620

QY 232 TyrAsnLeuValProSerAsnTyrPglInPheGlyGlnThrTyrGlyGlyProGlnPhe 250
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Db 1621 TACAATGTAGTGCCTGCTGTGTGCAATTGCGACAACTTTTGAAGAGGCGCAGTTT 1677

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RESULT 5

US-08-298-829-26

; Sequence 26, Application US/08298829

; Patent No. 5620882

; GENERAL INFORMATION:

; APPLICANT: John, Mallyakal E.

; TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON

; TITLE OF INVENTION: PLANTS FOR ALTERED FIBER

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Nicholas J. Seay, Quarles & Brady

; STREET: P. O. Box 2113, First Wisconsin Plaza

; CITY: Madison

; STATE: Wisconsin

; COUNTRY: USA

; ZIP: 53701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Microsoft word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/298,829

; FILING DATE: 19-OCT-1994

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/885,970

; FILING DATE: 18-MAY-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/617,239

; FILING DATE: 21-NOV-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/253,243

; FILING DATE: 04-OCT-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Seay, Nicholas J.

; REGISTRATION NUMBER: 27,386

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (608) 283-2478

; TELEFAX: (608) 251-5139

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2415 base pairs

; TYPE: nucleic acid

STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Gossypium barbadense
 STRAIN: Sea Island
 IMMEDIATE SOURCE:
 LIBRARY: EMBL-SI
 CLONE: SIB12
 US-08-298-829-26

Alignment Scores:
 Pred. No.: 3.13e-95 Length: 2415
 Score: 919.50 Matches: 184
 Percent Similarity: 70.43% Conservative: 28
 Best Local Similarity: 61.13% Mismatches: 36
 Query Match: 65.96% Indels: 56
 DB: 1 Gaps: 2

US-09-383-579c-10 (1-250) x US-08-298-829-26 (1-2415)

QY 3 PheSerTyrSerProPheSerSerLeuPheLeuProPhePheValPheThrPhe 22
 DB 784 TTTCACCTTCTCTCTTTTGTTCAGTGTATGCAACTCCATTTCTTGCTATATGA- 842
 QY 23 AlaAspTyrGlyGlyTyrPheSerGlyHisAlaThrPheTyrGlyGlyAspAlaSer 42
 DB 843 GATGACAATGGTGGTTG-CAAACTGCCCATGC-ACCTTCTACGGTGGTGTGATGCTACC 900
 QY 43 GlyThrMet----- 45
 DB 901 GGCACAATGGGTGAGTTCAAACTTCAAAACATTACCTACATAAAATCTCTAGGCTAT 960
 QY 46 -----GlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGly 57
 DB 961 GTTCTTAATTTGTGATGTTCTATAGGGGAGCTTGTGTTATGAAACCTGTACAGTCA 1020
 QY 57 nGlyTyrGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCy 77
 DB 1021 AGGGTATGGAACGACACAGCAGCAGCTTGTAGCACTTTCAACAATGGCTTGAGCTG 1080
 QY 77 sGlyAla-CysPheGlyMetThrCysThrAsnAspProLysTyrCysLeuProGlyThrI 97
 DB 1081 CGGTGACACTGCTACGAGCTCCGGTGCACAACATGATCCTCAATGGTGATGACGAACCA 1140
 QY 97 leArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnGlyG 117
 DB 1141 TAACCGTGACAGCCACCACTTTGTGTCCTTAATGCTTATCTAGTGAATGCGC 1200
 QY 117 lYTrpCysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleA 137
 DB 1201 GGTGTGCAATCCCCCAGAGAACACTTGTGATTTGGCCGACCGGCACTTTGCAAGATCG 1260
 QY 137 lagIntYrArgAlaGlyIleValProValSerPheArg----- 149
 DB 1261 CGGAATATCGAGCTGGAATCGCCCTGTATGTTCAAGAGGTGGTGAATAAACTCAATT 1320
 QY 150 -----ArgVal 151
 DB 1321 CAATATCATCACTCTTAAGSTATGTAACTGTGGGTGTTTAACCTTTTGCAAGGTG 1380
 QY 152 ProCysMetLysLysGlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeu 171
 DB 1381 TCATGTGTGAAGAAAGAGGACATCAGGTACACCATGAATGGACATTCTGACTTCAACATG 1440
 QY 172 ValLeuIleThrAsnValGlyGlyAlaGlyAspValHisSerValSerIleLysGlySer 191
 DB 1441 GTGTGATTAACCAACGTGGGAGGGGAGGGGATATAACGTCACTGTCCATCAAGTGTCC 1500
 QY 192 ArgThrGlyTyrPheGlnSerMetSerArgAsnTyrPheGlnAsnTyrPheGlnSerAsnTyr 211

DB 1501 AAAACAGATGGCTACCTATGTCCAGAAATTGGGGCCAAACTGGCAGACAAATGCTTAC 1560
 QY 212 LeuAsnGlyGlnGlyLeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAla 231
 DB 1561 CTTAAGGCCAAAGCCTCTCTTTCAAAGTGACTGCCAGCATGGCAGACTATCACAAAC 1620
 QY 232 TyrAsnLeuValProSerAsnTyrPheGlnPheGlyGlnThrTyrGlyGlyProGlnPhe 250
 DB 1621 TACAATGTAGTGCCTGCTGTTGGCAATTCGACAACTTTGAAGAGGCCAGTTT 1677

RESULT 6

US-09-362-642-1
 ; Sequence 1, Application US/09362642
 ; Patent No. 6350935
 ; GENERAL INFORMATION:
 ; APPLICANT: Bennett, Alan B.
 ; APPLICANT: Rose, Jocelyn K.C.
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
 ; FILE REFERENCE: 023070-078210US
 ; CURRENT APPLICATION NUMBER: US/09/362,642
 ; CURRENT FILING DATE: 1999-07-27
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 702
 ; TYPE: DNA
 ; ORGANISM: Lycopersicon esculentum cv. T5
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (28)..(702)
 ; OTHER INFORMATION: tomato expansin (Lex1)
 US-09-362-642-1

Alignment Scores:
 Pred. No.: 4.09e-87 Length: 702
 Score: 841.50 Matches: 149
 Percent Similarity: 77.48% Conservative: 23
 Best Local Similarity: 67.12% Mismatches: 31
 Query Match: 60.37% Indels: 19
 DB: 4 Gaps: 3

US-09-383-579c-10 (1-250) x US-09-362-642-1 (1-702)

QY 13 LeuLeuProPhePhePheValPheThrPheAlaAspTyr----- 25
 DB 34 ATCATATTTTCATCCTGTTCTTCTTTGTAGACTCATGTTTCAACATTGTTGAAGGA 93
 QY 26 -----GlyGlyTyrPheGlnSerGlyHisAlaThrPheTyrGly 37
 DB 94 AGAATCCCTGGTGTCTTACTCTGCTGCTGATGGGAAACTGCACATGCTATTTACGGC 153
 QY 38 GlyGlyAspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGln 57
 DB 154 GGAAGTATGCTTCTGGAACAATGGCGGCTGCTGTTATGAAATTATACAGCCAA 213
 QY 58 GlyTyrGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCys 77
 DB 214 GGATACGGAGTTAACACACAGCACTAGTACTGCTTGTTTAACAATGATTAAGTTGT 273
 QY 78 GlyAlaCysPheGlyMetThrCysThrAsnAspPro-----LysTyrCysLeuProGly 95
 DB 274 GGAGCCTGTTTGAACCTTAATGTAACAATACTCTTAATTTGGAATGGTGTCTTCTGCA 333
 QY 96 -----ThrIleArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsn 113
 DB 334 AACCTTTCATTTTAATACACAGCTACCAATTTCTGCCCAACCAATTACCGGTTGCCAAAT 393
 QY 114 AsnAsnGlyGlyTyrCysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPhe 133
 DB 394 GACAAATGGTGGTGTGTGAACCTCTCGCCCTCACTTGAACCTGCTATGCTATGCTT 453

QY 134 LeuGlnIleAlaGlnTyrArgAlaGlyIleValProValSerPheArgValProCys 153
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 Db 454 CTCAACTTGTCTCAGTACCGCGCTGGCATTTCTCTGTAACCTATATCCAGATCCCATGC 513
 QY 154 MetIysLysGlyGlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeu 173
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 Db 514 CGAAGCAAGAGAGATCAGATTACATCAATGATTCGTTACTTCAACTAGTGTG 573
 QY 174 IleThrAsnValGlyGlyAlaGlyAspValHisSerValSerIleLysGlySerArgThr 193
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 Db 574 ATCAGCAATGTAGACGTGCAGGGGATATTATTAGGTTGGTAAAGAACAAAGACA 633
 QY 194 GlyTrrGlnSerMetSerArgAsnTrrGlyGlnAsnTrrGlnSerAsnAsnTrrLeuAsn 213
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 Db 634 AATTGGATTGCATTGAGCCGTAATTGGGGACAAATGGCAATCAATGCGGTTTAACT 693
 QY 214 GlyGln 215
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 Db 694 GGTCAA 699

RESULT 7

US-08-845-539-1
 ; Sequence 1, Application US/08845539
 ; Patent No. 5929303
 ; GENERAL INFORMATION:
 ; APPLICANT: Bennett, Alan B.
 ; APPLICANT: Rose, Jocelyn K.C.
 ; TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
 ; TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/845,539
 ; FILING DATE: 25-APR-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Baetian, Kevin L.
 ; REGISTRATION NUMBER: 34,774
 ; REFERENCE/DOCKET NUMBER: 023070-078200US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 702 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 28..702
 ; OTHER INFORMATION: /product= "tomato LeEx1"
 ; US-08-845-539-1

Alignment Scores:
 Pred. No.: 6.93e-87 Length: 702
 Score: 839.50 Matches: 149
 Percent Similarity: 77.03% Conservative: 22
 Best Local Similarity: 67.12% Mismatches: 32
 Query Match: 60.22% Indels: 19
 DB: 2 Gaps: 3

US-09-383-579c-10 (1-250) x US-08-845-539-1 (1-702)

QY 13 LeuLeuProPhePhePheValPheThrPheAlaAspTyr----- 25
 ::::|||||
 Db 34 ATCATATATTTCATCTCTGTTCTTTGTAGACTCATGTTTCAACATTGTGAAGGA 93
 QY 26 -----GlyGlyTrrGlnSerGlyHisIleAlaThrPheTyrGly 37
 |||:::|||||
 Db 94 AGATCCCTGCTGTCTTACTCTGGGGTTCATGGGAACTGCACATGCTACATTTTACGGC 153
 QY 38 GlyGlyAspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGln 57
 |||:::|||||
 Db 154 GGAAGTGAATGCTTCTGGAACAATGGCGGTGCGGTGTTATGGAATTATACGCCAA 213
 QY 58 GlyTyrGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCys 77
 |||:::|||||
 Db 214 GGATACCGAGTTTAAACACAGCAGCACTGAGTACTGCTTGTTTAACAATGATTAAGTTGT 273
 QY 78 GlyAlaCysPheGluMetThrCysThrAsnAspPro-----LysTrrCysLeuProGly 95
 |||:::|||||
 Db 274 GGAGCTGTTTGAACCTTAATGTACAAATACTCTTAATGGAAATGCTGCTCTCGGA 333
 QY 96 -----ThrIleArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsn 113
 ::::|||||
 Db 334 AACCTTCCATTTTAATCACAGCTTACCAATTTCTGCCACCAATTAACGCGTTGCCAAAT 393
 QY 114 AsnAsnGlyGlyTrrCysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPhe 133
 ::::|||||
 Db 394 GACAAATGGTGGCTGGTGTAAACCTCTCGCCCTCACTTGACCTCGCTATGCTTATGTTT 453
 QY 134 LeuGlnIleAlaGlnTyrArgAlaGlyIleValProValSerPheArgValProCys 153
 |||:::|||||
 Db 454 CTCAACTTGTCTCAGTACCGCGCTGGCATTTCTCTGTAACCTATATCCAGATCCCATGC 513
 QY 154 MetIysLysGlyGlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeu 173
 |||:::|||||
 Db 514 CGAAGCAAGAGAGATCAGATTACATCAATGATTCGTTACTTCAACTAGTGTG 573
 QY 174 IleThrAsnValGlyGlyAlaGlyAspValHisSerValSerIleLysGlySerArgThr 193
 |||:::|||||
 Db 574 ATCAGCAATGTAGACGTGCAGGGGATATTATTAGGTTGGGTAAAGAACAAAGACA 633
 QY 194 GlyTrrGlnSerMetSerArgAsnTrrGlyGlnAsnTrrGlnSerAsnAsnTrrLeuAsn 213
 |||:::|||||
 Db 634 AATTGGATTGCATTGAGCCGTAATTGGGGACAAATGGCAATCAATGCGGTTTAACT 693
 QY 214 GlyGln 215
 |||:::|||||
 Db 694 GGTCAA 699

RESULT 8

US-08-845-539-5
 ; Sequence 5, Application US/08845539
 ; Patent No. 5929303
 ; GENERAL INFORMATION:
 ; APPLICANT: Bennett, Alan B.
 ; APPLICANT: Rose, Jocelyn K.C.
 ; TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
 ; TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30

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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/845,539
/ FILING DATE: 25-APR-1997
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bastian, Kevin L.
/ REGISTRATION NUMBER: 34,774
/ REFERENCE/DOCKET NUMBER: 023070-078200US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 537 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..537
/ OTHER INFORMATION: /product= "melon CmEx1"
US-08-845-539-5

Alignment Scores:
Pred. No.: 3.38e-82 Length: 537
Score: 797.00 Matches: 140
Percent Similarity: 86.44% Conservative: 13
Best Local Similarity: 79.10% Mismatches: 22
Query Match: 57.17% Indels: 2
DB: 2 Gaps: 1

US-09-383-579c-10 (1-250) x US-08-845-539-5 (1-537)
QY 33 AlaThrPheTyrGlyGlyGlyAspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGly 52
DB 7 GCCACGTTTATGAGGACGCGATGCTCCGGAACCATGGGTGGTCTTGCGGTATGCG 66
QY 53 AsnLeuTyrSerGlnGlyTyrGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsn 72
DB 67 AATCTCTACAGCCAGGCGCTATGGCTCAACACAGCTGCTTAGTACTGCTTCTTCAAC 126
QY 73 AsnGlyLeuSerCysGlyAlaCysPheGluMetThrCysThrAsnAspProLysTyrCys 92
DB 127 AATGGCTCAGCTGTGGTCTGCTTGTGAGATCAAGTGTCTAATGACCTCGATGTGC 186
QY 93 LeuProGlyThr-----IleArgValThrAlaThrAsnPheCysProProAsnPheAla 110
DB 187 CATCCTGTGAGCCCTGTATCTTCAATACCGCTACCAATTTTGTCCCTAACCTTGTCT 246
QY 111 LeuProAsnAsnAsnGlyGlyTyrCysAsnProProLeuGlnHisPheAspMetAlaGlu 130
DB 247 CTTCTTAATGACAATGGCGGTGGTGAACCTTCTCGCACTCATTTGACCTCGCTATG 306
QY 131 ProAlaPheLeuGlnIleAlaGlnTyrArgAlaGlyIleValProValSerPheArgArg 150
DB 307 CCTATGTTCTCAAGATCGCTGAGTACCGCGCTGAATCGACCTGTCTTACCGCGCG 366
QY 151 ValProCysMetLysLysGlyGlyValAlaArgPheThrIleAsnGlyHisSerTyrPheAsn 170
DB 367 GTTCCATGTAGGAACAAGAGGAATCAGGTTCAATCAACGAGTTTCCGTTACTTCAAT 426
QY 171 LeuValLeuIleThrAsnValGlyGlyAlaGlyAspValHisSerValSerIleLysGly 190
DB 427 TTGGTGTATATCAACCAACGTCGCGGTGACGGGATATCGTGAAGGTCAAGCAAAAGA 486
QY 191 SerArgThrGlyTyrGlnSerMetSerArgAsnTyrGlyGlnAsnTyrGln 207
DB 487 TCAAAACACCGGTTGGATGAGCATGAGTGTGTAATTGGGGCCAAACTGGCAG 537
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RESULT 9
US-09-362-642-5
; Sequence 5, Application US/09362642
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/ Patent No. 6350935
/ GENERAL INFORMATION:
/ APPLICANT: Bennett, Alan B.
/ APPLICANT: Rose, Jocelyn K.C.
/ APPLICANT: The Regents of the University of California
/ TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
/ TITLE OF INVENTION: to Control Fruit Texture and Softening
/ FILE REFERENCE: 023070-078210US
/ CURRENT APPLICATION NUMBER: US/09/362,642
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 537
/ TYPE: DNA
/ ORGANISM: Cucumis melo
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(537)
/ OTHER INFORMATION: melon expansin (CmEx1) partial cDNA clone
US-09-362-642-5

Alignment Scores:
Pred. No.: 3.38e-82 Length: 537
Score: 797.00 Matches: 140
Percent Similarity: 86.44% Conservative: 13
Best Local Similarity: 79.10% Mismatches: 22
Query Match: 57.17% Indels: 2
DB: 4 Gaps: 1

US-09-383-579c-10 (1-250) x US-09-362-642-5 (1-537)
QY 33 AlaThrPheTyrGlyGlyGlyAspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGly 52
DB 7 GCCACGTTTATGAGGACGCGATGCTCCGGAACCATGGGTGGTCTTGCGGTATGCG 66
QY 53 AsnLeuTyrSerGlnGlyTyrGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsn 72
DB 67 AATCTCTACAGCCAGGCGCTATGGCTCAACACAGCTGCTTAGTACTGCTTCTTCAAC 126
QY 73 AsnGlyLeuSerCysGlyAlaCysPheGluMetThrCysThrAsnAspProLysTyrCys 92
DB 127 AATGGCTCAGCTGTGGTCTGCTTGTGAGATCAAGTGTCTAATGACCTCGATGTGC 186
QY 93 LeuProGlyThr-----IleArgValThrAlaThrAsnPheCysProProAsnPheAla 110
DB 187 CATCCTGTGAGCCCTGTATCTTCAATACCGCTACCAATTTTGTCCCTAACCTTGTCT 246
QY 111 LeuProAsnAsnAsnGlyGlyTyrCysAsnProProLeuGlnHisPheAspMetAlaGlu 130
DB 247 CTTCTTAATGACAATGGCGGTGGTGAACCTTCTCGCACTCATTTGACCTCGCTATG 306
QY 131 ProAlaPheLeuGlnIleAlaGlnTyrArgAlaGlyIleValProValSerPheArgArg 150
DB 307 CCTATGTTCTCAAGATCGCTGAGTACCGCGCTGAATCGACCTGTCTTACCGCGCG 366
QY 151 ValProCysMetLysLysGlyGlyValAlaArgPheThrIleAsnGlyHisSerTyrPheAsn 170
DB 367 GTTCCATGTAGGAACAAGAGGAATCAGGTTCAATCAACGAGTTTCCGTTACTTCAAT 426
QY 171 LeuValLeuIleThrAsnValGlyGlyAlaGlyAspValHisSerValSerIleLysGly 190
DB 427 TTGGTGTATATCAACCAACGTCGCGGTGACGGGATATCGTGAAGGTCAAGCAAAAGA 486
QY 191 SerArgThrGlyTyrGlnSerMetSerArgAsnTyrGlyGlnAsnTyrGln 207
DB 487 TCAAAACACCGGTTGGATGAGCATGAGTGTGTAATTGGGGCCAAACTGGCAG 537
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RESULT 10
US-08-845-539-3
; Sequence 3, Application US/08845539
; Patent No. 5929303
; GENERAL INFORMATION:
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; APPLICANT: Bennett, Alan B.
 ; APPLICANT: Rose, Jocelyn K.C.
 ; TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
 ; TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/845,539
 ; FILING DATE: 25-APR-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bastian, Kevin L.
 ; REGISTRATION NUMBER: 34,774
 ; REFERENCE/DOCKET NUMBER: 023070-078200US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 501 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..501
 ; OTHER INFORMATION: /product= "strawberry FaEx1"
 ;
 ; US-08-845-539-3

Alignment Scores:
 Pred. No.: 8.37e-75 Length: 501
 Score: 732.00 Matches: 127
 Percent Similarity: 85.63% Conservative: 16
 Best Local Similarity: 76.05% Mismatches: 22
 Query Match: 52.51% Indels: 2
 DB: 2 Gaps: 1

US-09-383-579c-10 (1-250) x US-08-845-539-3 (1-501)

QY 43 G|YThrMetG|G|Y|A|A|C|Y|S|G|Y|T|Y|G|Y|A|S|N|L|E|U|T|Y|R|S|E|G|I|N|G|Y|T|Y|G|Y|T|H|A|S|N 62
 DB 1 GGAACCATGGGGGGTGTGTTGATATGAAACCTTACAGCCAGGGCTACGGAGTCAAC 60
 QY 63 ThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGlu 82
 DB 61 ACTGCTGCGCTGAGCAGCGGCTCTGTTCAACAATGGCTGAGCTGCGGCTTGTTCAG 120
 QY 83 MetThrCysThrAsnAspProLysTrpCysLeuProGly-----ThrIleArgValThr 100
 DB 121 ATCAAGTGGCGGAGCAGCACCAGGTGGTGCAGTCCGGAAGCCCTTCATTTTCGTCAAC 180
 QY 101 AlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTrpCysAsn 120
 DB 181 GCCACCAACTTCTGCTCCCAACTTCTGCTCAGCCGACGACCAATGGCGTGTGTCAAC 240
 QY 121 ProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTrpArg 140
 DB 241 CCTCCCGGAGCCACTTGGACCTTGCATGCCCATGTTCTCAAGATGCCGAGTACAA 300
 QY 141 AlaGlyIleValProValSerPheArgArgValProCysMetLysLysGlyGlyValArg 160

DB 301 GCCGGAATGTCCTCCGCTCTTTACCCGCGGGTCCCATGCGTAAGAAGGTGGATCAGG 360
 QY 161 PheThrIleAsnGlyHisSerTyRPhAsnLeuValIleThrAsnValGlyGlyAla 180
 DB 361 TTCACATCAACGGCCACCAAGTACTTCAACCTGTTCTGATCACCACGTCGGCGGCGCA 420
 QY 181 GlyAspValHisSerValSerIleLeuGlySerArgThrGlyTrpGlnSerMetSerArg 200
 DB 421 GGGGATATCGTGAAGCGTGAAGCGGTAAGGACCAACACCGGGTGAATGCCAATGAGCCGA 480
 QY 201 AsnTrpGlyGlnAsnTrpGln 207
 DB 481 AATTGGGGTCAAACTGGCAG 501

RESULT 11
 US-09-362-642-3
 ; Sequence 3, Application US/09362642
 ; Patent No. 6350935
 ; GENERAL INFORMATION:
 ; APPLICANT: Bennett, Alan B.
 ; APPLICANT: Rose, Jocelyn K.C.
 ; TITLE OF INVENTION: The Regents of the University of California
 ; TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
 ; FILE REFERENCE: 023070-078210US
 ; CURRENT APPLICATION NUMBER: US/09/362,642
 ; CURRENT FILING DATE: 1999-07-27
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 501
 ; TYPE: DNA
 ; ORGANISM: Fragaria x ananassa
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(501)
 ; OTHER INFORMATION: strawberry expansin (FaEx1) partial cDNA clone
 ;
 ; US-09-362-642-3

Alignment Scores:
 Pred. No.: 8.37e-75 Length: 501
 Score: 732.00 Matches: 127
 Percent Similarity: 85.63% Conservative: 16
 Best Local Similarity: 76.05% Mismatches: 22
 Query Match: 52.51% Indels: 2
 DB: 4 Gaps: 1

US-09-383-579c-10 (1-250) x US-09-362-642-3 (1-501)

QY 43 G|YThrMetG|G|Y|A|A|C|Y|S|G|Y|T|Y|G|Y|A|S|N|L|E|U|T|Y|R|S|E|G|I|N|G|Y|T|Y|G|Y|T|H|A|S|N 62
 DB 1 GGAACCATGGGGGGTGTGTTGATATGAAACCTTACAGCCAGGGCTACGGAGTCAAC 60
 QY 63 ThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGlu 82
 DB 61 ACTGCTGCGCTGAGCAGCGGCTCTGTTCAACAATGGCTGAGCTGCGGCTTGTTCAG 120
 QY 83 MetThrCysThrAsnAspProLysTrpCysLeuProGly-----ThrIleArgValThr 100
 DB 121 ATCAAGTGGCGGAGCAGCACCAGGTGGTGCAGTCCGGAAGCCCTTCATTTTCGTCAAC 180
 QY 101 AlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTrpCysAsn 120
 DB 181 GCCACCAACTTCTGCTCCCAACTTCTGCTCAGCCGACGACCAATGGCGTGTGTCAAC 240
 QY 121 ProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTrpArg 140
 DB 241 CCTCCCGGAGCCACTTGGACCTTGCATGCCCATGTTCTCAAGATGCCGAGTACAA 300
 QY 141 AlaGlyIleValProValSerPheArgArgValProCysMetLysLysGlyGlyValArg 160
 DB 301 GCCGGAATGTCCTCCGCTCTTACCGCGGGTCCCATGCGTAAAGAAGGTGGATCAGG 360

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QY      161 PhetThrIleasnGlyHisSerTyrPheasnLeuValLeuIleThraSnValGlGlyAla 180
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Db      361 TTCACATCAACGCCACAAGTACTTCACCTGGTTCTCATCACCACCGTGCCGGCCGA 420

QY      181 GlyAspValHisSerValSerIleGlySerArgThrGlyTrpGlnSerMetSerArg 200
        |||||:::|||||:::|||||:::|||||:::|||||
Db      421 GGGGATATCGTAGCGGTGAGCGTGAAGAAGCACCAACACCGGGTGATGCCAATGAGCCGA 480

QY      201 AsnTrpGlyGlnAsnTrpGln 207
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Db      481 AATTGGGTCAAACCTGGCAG 501

RESULT 12
US-07-885-970A-6
; Sequence 6, Application US/07885970A
; Patent No. 5495070
; GENERAL INFORMATION:
; APPLICANT: John, Maliyakal E.
; TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nicholas J. Seay, Charles & Brady
; STREET: P.O. Box 2113, First Wisconsin Plaza
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/885,970A
; FILING DATE: 19920518
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/617,239
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/253,243
; FILING DATE: 04-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 283-2478
; TELEFAX: (608) 251-5139
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 727 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Gossypium hirsutum
; STRAIN: Coker 312
; DEVELOPMENTAL STAGE: 10 day old fiber cells
; TISSUE TYPE: fiber cells
; IMMEDIATE SOURCE:
; LIBRARY: CKFB10
; CLONE: B12
; US-07-885-970A-6

Alignment Scores:
Pred. No.:          1.39e-71          Length:          727
Score:              706.00             Matches:         123
Percent Similarity: 91.56%             Conservative:    18
Best Local Similarity: 79.87%           Mismatches:     13
Query Match:        50.65%             Indels:         0
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	US-09-383-579C-10	(1-250)	x	US-07-885-970A-6	(1-727)		
QY							
Db	1	IleArGValThrAlaThrAsnPhcysProProAsnPheAlaLeuProAsnAsnngly	116				
QY	117	GLYTrPCySasNPProLeuglnHisPheaspMelaGluproAlaPheLeuglnile	136				
Db	61	GGGTGTGCATCCCCCACAGACAACATTGAITTTGGCCGAACC GGCACTTCTTGCGATA	120				
QY	137	AlaGlnTyrrArgAlaGlyIleValProValSerPheaRgArgValProcysMetLysls	156				
Db	121	GCAGAATATCGAGCTGGAATCGTCCTGTATTATGTTCAGAAGGGTGTCGTGTGAAGAA	180				
QY	157	GlyGlyValArgPheThrIleasnGlyHisSerTyrrPheAsnLeuValleuIleThrAsn	176				
Db	181	GGAGGCATCAGTAACACCATGATGACATTCGTACTTCAACATGTTGTTGATTAACGAAC	240				
QY	177	VAlGIylglYAlaGlyAspValHIsSeRValserllelsgLyserAtqThrglyTryGln	196				
Db	241	GtGGAGGGGGCAGGGGATATAACGTCAGTGTCCATCAAGGGTTCAGAACAGGATGGCTA	300				
QY	197	SermetSerArgAsnTrpglyGlnAsnTrpgInserAsnsntTyrlEuasnGlyGlnGly	216				
Db	301	CCTATGTCAGAAATTGGGGCCAACCTGGCAGAGCAATGCTTACTTAAACGACAAAGC	360				
QY	217	LeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThralaTyrrAsnLeuValPro	236				
Db	361	CTCTCTTTAAAGTAGTACTGCCAGCGATGGCAGACTATCACAGCCTTACATGTAGTGCT	420				
QY	237	SerasnTrpgInPheGlyGlnThrtyrGluGlyProGlnPhe	250				
Db	421	GCTGCTGGCAAATTCGACAAACTTTGAAGGAGGCCAGTTT	462				
	RESULT 13						
	US-08-298-687A-6						
	; Sequence 6, Application US/08298687A						
	; Patent No. 5521078						
	: GENERAL INFORMATION:						
	: APPLICANT: John, Maliyakal E.						
	: TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON						
	: TITLE OF INVENTION: PLANTS FOR ALTERED FIBER						
	: NUMBER OF SEQUENCES: 33						
	: CORRESPONDENCE ADDRESS:						
	: ADDRESSEE: Nicholas J. Seay, Quarles & Brady						
	: STREET: P.O. Box 2113, First Wisconsin Plaza						
	: CITY: Madison						
	: STATE: Wisconsin						
	: COUNTRY: USA						
	: ZIP: 53701						
	: COMPUTER READABLE FORM:						
	: MEDIUM TYPE: Floppy disk						
	: COMPUTER: IBM PC compatible						
	: OPERATING SYSTEM: PC-DOS/MS-DOS						
	: SOFTWARE: Microsoft Word						
	: CURRENT APPLICATION DATA:						
	: APPLICATION NUMBER: US/08/298,687A						
	: FILING DATE:						
	: CLASSIFICATION: 800						
	: PRIOR APPLICATION DATA:						
	: APPLICATION NUMBER: US 07/617,239						
	: FILING DATE: 21-NOV-1990						
	: PRIOR APPLICATION DATA:						
	: APPLICATION NUMBER: US 07/253,243						
	: FILING DATE: 04-OCT-1988						
	: ATTORNEY/AGENT INFORMATION:						
	: NAME: Seay, Nicholas J.						
	: REGISTRATION NUMBER: 27,386						
	: TELECOMMUNICATION INFORMATION:						
	: TELEPHONE: (608) 283-2478						
	: TELEFAX: (608) 251-5139						

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/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 727 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Gossypium hirsutum
/ STRAIN: Coker 312
/ DEVELOPMENTAL STAGE: 10 day old fiber cells
/ TISSUE TYPE: fiber cells
/ IMMEDIATE SOURCE:
/ LIBRARY: CKFB10
/ CLONE: B12
/ US-08-298-687A-6

Alignment Scores:
Pred. No.: 1.39e-71 length: 727
Score: 706.00 Matches: 123
Percent Similarity: 91.56% Conservative: 18
Best Local Similarity: 79.87% Mismatches: 13
Query Match: 50.65% Indels: 0
DB: 1 Gaps: 0

US-09-383-579c-10 (1-250) x US-08-298-687A-6 (1-727)
QY 97 IleaRgValThraIaThraSnpheCysProProAsnPhaAlaLeuProAsnAsnAngly 116
Db 1 ATACCCTGACAGCCACCACCTTTGTGTCACCTACTATGCTTATCTAGTGACCAATGGC 60
QY 117 GLyTTPCySAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIle 136
Db 61 GGGTGTGCAATCCCCCAGAGAACACTTTGATTGGCCGAACCGGCAATCTTGCGGATA 120
QY 137 AlaGlnTyraGAlaGlyIleValProValSerPheArgValProCysMetLysLys 156
Db 121 GCAGAAATATCGAGCTGGAATCGTCCCTGTATGTTCAGAAAGGGTGTGATGTGAAGAAA 180
QY 157 GLyGlyValArgPheThrIleAsnGlyHisSerTyrrPheAsnLeuValIleThraSn 176
Db 181 GGAGGCATCAGGTACACCATGAATGACATTGCTACTTCAACATGGTGTGATTAACGAAAC 240
QY 177 ValGlyGlyAlaGlyAspValHisSerValSerIleLysGlySerArgThrGlyTTPGln 196
Db 241 GTGGAGGGGCGAGGGGATATTAACGTGATGTCATCAAGGGTTCAGAAACAGATGGCTA 300
QY 197 SerMetSerArgAsnTTPGlyGlnAsnTTPGlnSerAsnAsnTyrrLeuAsnGlyGlnGly 216
Db 301 CCTATGTCAGAAATGGGGCCAAACATGGCAGAGCAATGCTTACCTTAACGAGCAAAAC 360
QY 217 LeuSerPheGlnValThrLeuSerArgPGLYArgThrLeuThraIaTyrrAsnLeuValPro 236
Db 361 CTCTCTTTTAAAGTGACTGCCAGCGATGGCAGAGACTATCACAGCCTTAACATGTAGTCCCT 420
QY 237 SerAsnTTPGlnPheGlyGlnThrTyrrGlyGlyProGlnPhe 250
Db 421 GCTGTGTGGCAATTCGACAAACTTTGAAGAGGCGCAGTTT 462

RESULT 14
US-08-530-797-5
/ Sequence 5, Application US/08530797
/ Patent No. 5597718
/ GENERAL INFORMATION:
/ APPLICANT: John, Maliyakal E.
/ APPLICANT: Umbeck, Paul F.
/ APPLICANT: Brill, Winston J.
/ TITLE OF INVENTION: GENETICALLY ENGINEERED COTTON PLANTS
/ TITLE OF INVENTION: FOR ALTERED FIBER
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
```

```
/ ADDRESSEE: Quarles and Brady
/ STREET: P.O. BOX 2113
/ STREET: FIRST WISCONSIN PLAZA
/ CITY: MADISON
/ STATE: WISCONSIN
/ COUNTRY: U.S.A.
/ ZIP: 53701
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette - 3.50 inch, 800Kb storage
/ COMPUTER: Apple Macintosh
/ OPERATING SYSTEM: Macintosh
/ SOFTWARE: Microsoft Word 4.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/530,797
/ FILING DATE: 20-SEP-1995
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/617,239
/ FILING DATE: 21-NOV-90
/ APPLICATION NUMBER: US 07/253,243
/ FILING DATE: 04-OCT-88
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Nicholas J. Seay
/ REGISTRATION NUMBER: 27,386
/ REFERENCE/DOCKET NUMBER: 1122990245
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 727 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ HYPOTHETICAL: no
/ ANTI-SENSE: no
/ ORIGINAL SOURCE:
/ ORGANISM: Gossypium hirsutum
/ STRAIN: Coker 312
/ DEVELOPMENTAL STAGE: 10 day old fiber cells
/ TISSUE TYPE: fiber cells
/ IMMEDIATE SOURCE:
/ LIBRARY: CKFB10
/ CLONE: B12
/ US-08-530-797-5

Alignment Scores:
Pred. No.: 1.39e-71 length: 727
Score: 706.00 Matches: 123
Percent Similarity: 91.56% Conservative: 18
Best Local Similarity: 79.87% Mismatches: 13
Query Match: 50.65% Indels: 0
DB: 1 Gaps: 0

US-09-383-579c-10 (1-250) x US-08-530-797-5 (1-727)
QY 97 IleaRgValThraIaThraSnpheCysProProAsnPhaAlaLeuProAsnAsnAngly 116
Db 1 ATACCCTGACAGCCACCACCTTTGTGTCACCTACTATGCTTATCTAGTGACCAATGGC 60
QY 117 GLyTTPCySAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIle 136
Db 61 GGGTGTGCAATCCCCCAGAGAACACTTTGATTGGCCGAACCGGCAATCTTGCGGATA 120
QY 137 AlaGlnTyraGAlaGlyIleValProValSerPheArgArgValProCysMetLysLys 156
Db 121 GCAGAAATATCGAGCTGGAATCGTCCCTGTATGTTCAGAAAGGGTGTGATGTGAAGAAA 180
QY 157 GLyGlyValArgPheThrIleAsnGlyHisSerTyrrPheAsnLeuValIleThraSn 176
Db 181 GGAGGCATCAGGTACACCATGAATGACATTGCTACTTCAACATGGTGTGATTAACGAAAC 240
QY 177 ValGlyGlyAlaGlyAspValHisSerValSerIleLysGlySerArgThrGlyTTPGln 196
Db 241 GTGGAGGGGCGAGGGGATATTAACGTGATGTCATCAAGGGTTCAGAAACAGATGGCTA 300
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QY 197 SerMetSerArgAsnTrpGlyGlnAsnTrpGlnSerAsnAsnTrpLeuAsnGlyGlnGly 216
Db 301 CCTATGTCCAGAAATTGGGGCCAAACTGGCAGACCAATGCTTACCTTAACGACCAAGC 360
QY 217 LeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValPro 236
Db 361 CTCTCTTTTAAGTACTGCCAGCGATGGCAGACTATCACAGCCTACAACTGTAAGTGCCT 420

QY 237 SerAsnTrpGlnPheGlyGlnThrTyrGlyGlnProGlnPhe 250
Db 421 GCTGTTGGCAATTCGACCAACTTTTGAAGAGGCCAGTTT 462

RESULT 15
US-08-298-829-6
; Sequence 6, Application US/08298829
; Patent No. 5620882
; GENERAL INFORMATION:
; APPLICANT: John, Maliyakal E.
; TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
; TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nicholas J. Seay, Quarles & Brady
; STREET: P.O. Box 2113, First Wisconsin Plaza
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/298,829
; FILING DATE: 19-OCT-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/885,970
; FILING DATE: 18-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/617,239
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/253,243
; FILING DATE: 04-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 283-2478
; TELEFAX: (608) 251-5139
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 727 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Gossypium hirsutum
; STRAIN: Coker 312
; DEVELOPMENTAL STAGE: 10 day old fiber cells
; TISSUE TYPE: fiber cells
; IMMEDIATE SOURCE:
; LIBRARY: CKFB10
; CLONE: B12
; US-08-298-829-6

Alignment Scores:

	Pred. No.:	1,39e-71	Length:	727
	Score:	706.00	Matches:	123
	Percent Similarity:	91.56%	Conservative:	18
	Best Local Similarity:	79.87%	Mismatches:	13
	Query Match:	50.65%	Indels:	0
	DB:	1	Gaps:	0

US-09-383-579c-10 (1-250) x US-08-298-829-6 (1-727)

QY 97 IleArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnGly 116
Db 1 ATAACCGTACAGCCACCACCACTTTGTCCACCTAACTATGCTTATCTAGTCAATGCC 60

QY 117 GlyTrpCysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIle 136
Db 61 GGGTGTGCAATCCCCACGAGAACACTTTGATTTGGCCGAACCGCATTTCTGCGGATA 120

QY 137 AlaGlnTrpArgAlaGlyIleValProValSerPheArgArgValProCysMetLysLys 156
Db 121 GCAGATATTCAGACTGGAATCGTCCCTGTATGTTGAGAAAGGTGTGATGTAAGAAA 180

QY 157 GlyGlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsn 176
Db 181 GGAGCATCAGGTACACCAATGATGACATCTTCAACATGTTGATGTAACGAAC 240

QY 177 ValGlyValAlaGlyAspValHisSerValSerIleLeuGlySerArgThrGlyTrpGln 196
Db 241 GTGGAGGGGAGGATATTAACGTCACTGTCATCAAGGTTCCAGAACAGATGGCTA 300

QY 197 SerMetSerArgAsnTrpGlyGlnAsnTrpGlnSerAsnAsnTrpLeuAsnGlyGlnGly 216
Db 301 CCTATGTCCAGAAATTGGGGCCAAACTGGCAGACCAATGCTTACCTTAACGACCAAGC 360

QY 217 LeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValPro 236
Db 361 CTCTCTTTTAAGTACTGCCAGCGATGGCAGACTATCACAGCCTACAACTGTAAGTGCCT 420

QY 237 SerAsnTrpGlnPheGlyGlnThrTyrGlyGlnProGlnPhe 250
Db 421 GCTGTTGGCAATTCGACCAACTTTTGAAGAGGCCAGTTT 462

Search completed: December 19, 2003, 01:04:20
Job time : 88 secs

GenCore version 5.1.6
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Run on: December 19, 2003, 00:28:28 ; Search time 292 Seconds

(without alignments)
2852.914 Million cell updates/sec

Title: US-09-383-579C-10

Perfect score: 1394
Sequence: 1 MAFSYPFSSSLFLLPFFV...AYNLVPSNMQFGQTEGPOF 250

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 221978 seqs, 1666101734 residues

Total number of hits satisfying chosen parameters: 4423956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnbp -MINMATCH=0.1
-LOOPL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09383579 @CGN 1 1.107 @runat_18122003_171929_28889
-NCPU=6 -ICPU=3 -NO_MMAL -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	1275	91.5	681	10	US-09-896-301-1	Sequence 1, Appli
2	1085	77.8	762	10	US-09-938-842A-1088	Sequence 1088, Ap
3	1044	74.9	1153	13	US-10-150-559-3	Sequence 3, Appli
4	1036.5	74.4	753	10	US-09-938-842A-91	Sequence 91, Appli
5	1027	73.7	759	13	US-10-409-701-8	Sequence 8, Appli
6	1024	73.5	747	10	US-09-938-842A-1069	Sequence 1069, Appli
7	993	71.2	774	10	US-09-938-842A-89	Sequence 89, Appli
8	939	67.4	774	10	US-09-938-842A-842	Sequence 842, App
9	938	67.3	893	9	US-09-770-445-491	Sequence 491, App
10	838.5	60.2	768	10	US-09-938-842A-1046	Sequence 1046, Ap
11	676	48.5	410	10	US-09-878-574-3973	Sequence 3973, Ap
12	643	46.1	391	10	US-09-878-574-62	Sequence 62, Appli
13	506	36.3	366	9	US-09-770-791-430	Sequence 430, App
14	491.5	35.3	373	10	US-09-878-574-3468	Sequence 3468, Ap
15	389.5	27.9	391	10	US-09-878-574-1206	Sequence 1206, Ap
16	294	21.1	1273	15	US-10-125-001-3	Sequence 3, Appli
17	288.5	20.7	293	9	US-09-294-093B-2002	Sequence 2002, Ap
18	276	19.8	1147	13	US-10-259-165-614	Sequence 614, App
19	271	19.4	810	13	US-10-259-165-776	Sequence 776, App
20	267.5	19.2	394	10	US-09-878-574-2728	Sequence 2728, Ap
21	266.5	19.1	1273	15	US-10-125-001-1	Sequence 1, Appli
22	266.5	19.1	1428	13	US-10-125-349-1	Sequence 15, Appli
23	262.5	18.8	735	15	US-10-409-701-10	Sequence 10, Appli
24	246	17.6	849	13	US-10-409-701-10	Sequence 10, Appli
25	240	17.2	262	10	US-09-878-574-14926	Sequence 14926, A
26	236.5	17.0	720	9	US-09-949-888-1	Sequence 1, Appli
27	230	16.5	285	10	US-09-878-574-13697	Sequence 13697, A
28	223	16.0	666	13	US-10-259-165-391	Sequence 391, App
29	223	16.0	669	13	US-10-259-165-43	Sequence 43, Appli
30	222.5	16.0	718	13	US-10-259-165-275	Sequence 275, App
31	206	14.8	798	10	US-09-938-842A-1951	Sequence 1951, App
32	196	14.1	259	10	US-09-878-574-12313	Sequence 12313, A
33	180.5	12.9	399	10	US-09-924-035A-461	Sequence 461, App
34	170.5	12.2	238	9	US-09-294-093B-4389	Sequence 4389, Ap
35	154.5	11.1	2536	13	US-10-102-349-3	Sequence 3, Appli
36	140	10.0	380	9	US-09-770-791-183	Sequence 183, App
37	139.5	10.0	279	9	US-09-294-093B-1776	Sequence 1776, Ap
38	126.5	9.1	277	10	US-09-878-574-8765	Sequence 8765, Ap
39	125.5	9.0	254	10	US-09-878-574-6584	Sequence 6584, Ap
40	122.5	8.8	275	10	US-09-878-574-6801	Sequence 6801, Ap
41	121	8.7	252	10	US-09-878-574-7975	Sequence 7975, Ap
42	119.5	8.6	1503	13	US-09-846-903-84	Sequence 84, Appli
43	118	8.5	264	10	US-09-878-574-5917	Sequence 5917, Ap
44	113	8.1	1952	15	US-10-197-294A-1	Sequence 1, Appli
45	103	7.4	852	13	US-10-259-165-652	Sequence 652, App

ALIGNMENTS

RESULT 1

US-09-896-301-1

Sequence 1, Application US/09896301

Patent No. US2002010355A1

GENERAL INFORMATION:

APPLICANT: Cosgrove, Daniel J

APPLICANT: McQueen-Mason, Simon

APPLICANT: Guiltinan, Mark J

APPLICANT: Shcherbar, Tatyana

APPLICANT: Shi, Jun

TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS

FILE REFERENCE: 1194/1C114US3

CURRENT APPLICATION NUMBER: US/09/896, 301

CURRENT FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: 09/092, 160

PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 08/440, 517

PRIOR FILING DATE: 1995-05-12

PRIOR APPLICATION NUMBER: 08/242, 090

PRIOR FILING DATE: 1994-05-12

PRIOR APPLICATION NUMBER: 08/060, 944

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 1
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA cucumber
; OTHER INFORMATION: expansin
US-09-896-301-1
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Alignment Scores:
Pred. No.: 1.92e-149 Length: 681
Score: 1275.00 Matches: 227
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 91.46% Indels: 0
DB: 10 Gaps: 0
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US-09-383-579C-10 (1-250) x US-09-896-301-1 (1-681)

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QY 24 AspTYRGLYGLYTRPGINSERGLYHISALATHRPHEFYRGLYGLYASPALASERGLY 43
DB 1 GACTACGGTGGCTGGCAGAGCGGCCACGCCACCTTTATAGTGTGTGACGCATCTGGC 60
QY 44 ThrMetGLYGLYALACYSGLYTYRGLYASNLEUTYRSEGLNGLYTYRGLYThraNThr 63
DB 61 ACCATGGGTGAGCTGTGGTATGGGAATTATACAGCCAAAGGGTATGGCAGCAACG 120
QY 64 ValAlaLeuSerThrAlaLeuPheAsnAsnGLYLeuSerCysGLYAlaCysPheGluMet 83
DB 121 GTGGCGCTGAGCACTGCGCTATTATCAATGATTAAGTTGTGTGCTTGTGCAATG 180
QY 84 ThrCysThrAsnAspProLYSTYRPGYLeuProGLYThrIleArgValThraLThraSn 103
DB 181 ACTTGATCAAAACGACCTTAATGGTGCTTCGCGGAATAATTAGGTCACGCCAAC 240
QY 104 PheCysProProAsnPheAlaLeuProAsnAsnAsnGLYTYRPGYAsnProProLeu 123
DB 241 TTTTGCCCTCTTAACCTTGTCTCTCTCAACAACAATGGTGGATGGTCAACCTCTCTC 300
QY 124 GlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTYRArgAlaGlyIle 143
DB 301 CAACACTTCGACATGGCTGAGCCCTGCTCTTCAATCGCTCAATACCGAGCTGTATC 360
QY 144 ValProValSerPheArgArgValProCysMetLYSGLYGLYValAlaArgPheThrIle 163
DB 361 GTCCCGCTCTCTTCGTAGGGTACCATGTATGAAGAAAGTGAAGTGAAGTTTACATC 420
QY 164 AsnGlnHisSerTYRPhaAsnLeuValLeuIleThrAsnValGLYGLYAlaGlyAspVal 183
DB 421 AATGGCCACTCATACTCAACCTCGTTTGTATCACAAACGTGGTGGCGCAGCGCTC 480
QY 184 HisSerValSerIleLYSGLYSerArgThrgLYTRPGINSERMetSerArgAsnTrpGly 203
DB 481 CACTGTGTGTGATTAAGGGGTCTCGAATCGATGGCAATCCATGTCTAGAAATGGGGC 540
QY 204 GlnAsnTrpGlnSerAsnAsnTYRLeuAsnGLYGLNGLYLeuSerPheGlnValThrLeu 223
DB 541 CAAACTGGCAAGCAACAATATCTCAATGGCCAGGCCCTTCTCTTCAAGTCACTCTT 600
QY 224 SerAspGLYArgThrLeuThraLTYRAsnLeuValProSerAsnTrpGlnPheGlyGln 243
DB 601 AGTGATGGTGGCACTCTCACTGCCCTAATAATCTGTTCTTCAATTTGGCAATTTGGCCA 660
QY 244 ThrTYRGLNGLYProGlnPhe 250
DB 661 ACCTATGAAGGCCCTCAATTC 681
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RESULT 2
US-09-938-842A-1088
; Sequence 1088, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
```

```
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227, 866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264, 647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300, 111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1088
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1088
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Alignment Scores:
Pred. No.: 1.25e-125 Length: 762
Score: 1085.00 Matches: 194
Percent Similarity: 86.75% Conservative: 22
Best Local Similarity: 77.91% Mismatches: 31
Query Match: 77.83% Indels: 2
DB: 10 Gaps: 2
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US-09-383-579C-10 (1-250) x US-09-938-842A-1088 (1-762)

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QY 4 SerTYRSeRProPheSerSerLeuPheLeuProPhePheVal---PheThrPhe 22
DB 13 TCATTACTTAATAATATTCATAATATCTCAATATATCCGATTATTCTCCAAAGAACTCAT 72
QY 23 AlaAspTYRGLYGLYTRPGINSERGLYHISALATHRPHEFYRGLYGLYASPALASER 42
DB 73 GGAGACGACGAGGTGGCAAGGTGGTCACGCCAGTTTACGGCGCGGAAGATGCTTCC 132
QY 43 GlnThrMetGLYGLYALACYSGLYTYRGLYASNLEUTYRSEGLNGLYTYRGLYThraSn 62
DB 133 GGCAACATGGCGGAGCTGTGGCTATGAAATTTGTATGGCCAGGTTACGGGACGAAC 192
QY 63 ThrValAlaLeuSerThrAlaLeuPheAsnAsnGLYLeuSerCysGLYAlaCysPheGlu 82
DB 193 ACGCGGCTTTAAGTACGGCTTATTCACAACAGCACTACAGTGGCGGTATGAG 252
QY 83 MetThrCysThrAsnAspProLYSTYRPGYLeuProGLYThrIleArgValThraLThr 102
DB 253 ATGAAGTGTACGATGACCCGAGGTGGTCTCGGGTCAACCATCACCGTACAGCTACA 312
QY 103 AsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGLYTYRPGYAsnProPro 122
DB 313 AACTTTGCCCACTTAACCTGCGCTCTCCAACGATATGAGGTGTGCAATCTCTCT 372
QY 123 LeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTYRArgAlaGly 142
DB 373 CTTGACGATTTGACCTCGCCGAGCCAGCTTTCTTCAATCGTCAATCGTCCGGC 432
QY 143 IleValProValSerPheArgArgValProCysMetLYSGLYGLYValAlaArgPheThr 162
DB 433 ATTGTCTGTCTCTTTCGGAAGGTATCCATGTATGAAGAAAGGAATTAAGTTTACG 492
QY 163 IleAsnGlnHisSerTYRPhaAsnLeuValLeuIleThrAsnValGLYGLYAlaGlyAsp 182
DB 493 ATCAACGAGACACTACTTCAACCTCGTTCTGATCTCCAACGTAAGAGAGAGAGAC 552
QY 183 ValHisSerValSerIleLYSGLYSerArgThr---GLYTRPGINSERMetSerArgAsn 201
DB 553 GTACACGCCGCTCTCAATCAAAAGGCTCAAAACACAGTCGTGCAAGCATGTCTGAAC 612
QY 202 TrpGLYGLNAsnTrpGlnSerAsnAsnTYRLeuAsnGLYGLNGLYLeuSerPheGlnVal 221
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Db 613 TGGGGACAAAAGCTGGCAGACAAATTCATACATGAACGACCAAGCCTTCTCCAGGTA 672
QY 222 ThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGlnPhe 241
Db 673 ACGACGACGATGGTGCACACACCTGTTAGCAACGACGTCCTCTTAATTGGCAGTTTC 732
QY 242 GtGlnThrTyrGlnGlyProGlnPhe 250
Db 733 GGACAAACCTACCAAGGTGTGAGTTTC 759

RESULT 3
US-10-150-559-3

/ Sequence 3, Application US/10150559
/ Publication No. US20030221218A1
/ GENERAL INFORMATION:
/ APPLICANT: Wilkins, Thea A.
/ APPLICANT: The Regents of the University of California
/ TITLE OF INVENTION: Bioengineering Cotton Fiber Properties
/ FILE REFERENCE: 023070-116500US
/ CURRENT APPLICATION NUMBER: US/10/150,559
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 1153
/ TYPE: DNA
/ ORGANISM: Gossypium hirsutum
/ FEATURE:
/ OTHER INFORMATION: expansin
US-10-150-559-3

Alignment Scores:

Pred. No.:	3.03e-120	Length:	1153
Score:	1044.00	Matches:	185
Percent Similarity:	85.48%	Conservative:	27
Best Local Similarity:	74.60%	Mismatches:	36
Query Match:	74.89%	Indels:	1
DB:	13	Gaps:	0

US-09-383-579C-10 (1-250) x US-10-150-559-3 (1-1153)

QY 3 PheSerTyrSerProPheSerSerLeuPheLeuLeuProPhePheValPheThrPhe 22
Db 78 TTTCACTTTCTCTTTTGTTCAGTATCTGCAACTCCATTTCTTGTGCTAATGA- 136
QY 23 AlaAspTyrGlyGlyTyrGlnSerGlyHisAlaThrPheTyrGlyGlyAspAlaSer 42
Db 137 GATGACAATGGTGGTGGCAAACTGCCATGCCCTTCTACGGTGTGCTGATGCTACC 196
QY 43 GlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsn 62
Db 197 GGCACAATGGGGGAGCTTGTGTTATGGAACCTGTACAGTCAAGGGTATGGAACGAGC 256
QY 63 ThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGlu 82
Db 257 ACAGCAGCTTTGAGCACTGCACCTTTCAACAATGGCTTGAGCTGCGGCTTCTACGAG 316
QY 83 MetThrCysThrAsnAspProLysTrpCysLeuProGlyThrIleArgValThrAlaThr 102
Db 317 CTCCGGTGCAACAATGATCTCTCAATGCTGATTAAGTGAACCAATACCCTGACAGCCACC 376
QY 103 AsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTyrCysAsnProPro 122
Db 377 AACTTTGTCTCCCTAATCTATCTTATCTAGTGAACAATGGGGGTGTGCAATCCCCCA 436
QY 123 LeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGly 142
Db 437 CGAGAACACTTTGATTTGGCCGCAACCGGCACTTCTTGACAGTCGGGAATATCGAGCTGGG 496
QY 143 IleValProValSerPheArgArgValProCysMetLysLysGlyGlyValArgPheThr 162
Db 497 ATCGTCCCTGTATTATGTTCAAGAGGGGTGTATGTGTAAGAAAGAGGCATCAGGTACACC 556

QY 163 IleAsnGlyHisSerTyrPheAsnLeuValIleThrAsnValGlyValAlaGlyAsp 182
Db 557 ATGATGACACTTCGTAATCAACATGCTGTGATAACCAACGTGGAGGGCAGGGAT 616
QY 183 ValHisSerValSerIleLysGlySerArgThrGlyTyrGlnSerMetSerArgAsnTrp 202
Db 617 ATAACGTCACTGTCATCAAGGTTCCAAACAGAGATGGCTTATGTCCGAATTCG 676
QY 203 GlyGlnAsnTrpGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGlnValThr 222
Db 677 GCCCAAACTGGCAGACGACATGCTTACCTTAACGCCCAAGCCTCTTCAAGTACT 736
QY 223 LeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGlnPheGly 242
Db 737 GCCAGCATACAGACTATCAACAACATGATAGTGCCTGCTGTGCAATTCCGA 796
QY 243 GlnThrTyrGlnGlyProGlnPhe 250
Db 797 CAACTTTGAAAGAGGCCAGTTT 820

RESULT 4

US-09-938-842A-91

/ Sequence 91, Application US/09938842A
/ Patent No. US20020160378A1
/ GENERAL INFORMATION:
/ APPLICANT: Harper, Jeff
/ APPLICANT: Krepes, Joel
/ APPLICANT: Wang, Xun
/ APPLICANT: Zhu, Tong
/ TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
/ FILE REFERENCE: SCRIPI300-3
/ CURRENT APPLICATION NUMBER: US/09/938,842A
/ PRIOR FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: US 60/227,866
/ PRIOR FILING DATE: 2000-08-24
/ PRIOR APPLICATION NUMBER: US 60/264,647
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/300,111
/ PRIOR FILING DATE: 2001-06-22
/ NUMBER OF SEQ ID NOS: 5379
/ SEQ ID NO 91
/ LENGTH: 753
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
US-09-938-842A-91

Alignment Scores:

Pred. No.:	1.41e-119	Length:	753
Score:	1036.50	Matches:	181
Percent Similarity:	83.74%	Conservative:	25
Best Local Similarity:	73.58%	Mismatches:	31
Query Match:	74.35%	Indels:	9
DB:	10	Gaps:	1

US-09-383-579C-10 (1-250) x US-09-938-842A-91 (1-753)

QY 13 LeuLeuProPhePhePheValPheThrPheAlaAspTyr----- 25
Db 7 CTGTCACTTCTTGTATTGCTTACCTTGAGCAATGACGTCAATGATGTTAC 66
QY 26 -----GtGlyTyrGlnSerGlyHisAlaThrPheTyrGlyGlyAspAlaSerGly 43
Db 67 GCCGAGAGGTTGGTGCAACGACACGCAATTCATGCGGTGTGATGCTTCCGGC 126
QY 44 ThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThr 63
Db 127 ACAATGGAGGTGCTGTGATACGGAACCTATATAGCCAAGGCTATGAAACCAACACG 186
QY 64 ValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGluMet 83
Db 187 GCGGCGCTAAGCACGCGCTCTATTCAATATATGTCTAAGTTGTGTGCTTCCGAGATA 246

QY 84 ThrCysThrAsnAspProLysTrpCysLeuProGlyThrIleArgValThrAlaThrAsn 103
Db 247 AGATGTCAAAACGATGAAAAATGGTGTCTTCTGGCTCAATTGTCTGACAGCCACAAAC 306
QY 104 PheCysProProAsnPhaAlaLeuProAsnAsnGlyGlyTrpCysAsnProProLeu 123
Db 307 TTTTGGCCCTCTTAACAACGCTTACCAACAACGAGAGGTTGGTTAAACCTCTCAG 366
QY 124 GlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTrpArgAlaGlyIle 143
Db 367 CAGCATTTTGTATCTCTCAGCCCGCTGATTCAACGATCGCTCAATTAACAGCCGCAAT 426
QY 144 ValProValSerPheArgArgValProCysMetLysGlyGlyValArgPheThrIle 163
Db 427 GTCCCGCTCGCTTACCGAAGAGTCCGTCGAGAGAGAGAAATAAGTTTACGATA 486
QY 164 AsnGlyHisSerTrpPheAsnLeuValLeuIleThrAsnValGlyGlyAlaGlyAspVal 183
Db 487 AACGACACTCTTACTTCAACCTAGTTCTGATCACTAACGTCGAGAGCCGAGATGTT 546
QY 184 HisSerValSerIleLysGlySerArgTrpGlyTrpGlnSerMetSerArgAsnTrpGly 203
Db 547 CACTCAGCGATGTTAAAGTTCAAGAACTGATGGCAAGCATGTCAAGAACTGGGGA 606
QY 204 GlnAsnTrpGlnSerAsnAsnTrpLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeu 223
Db 607 CAGAACTGGCAGAGTAATCTTACCTTAAACGACAATCTCTCATTAAGTTACACA 666
QY 224 SerAspGlyArgThrLeuThrAlaTrpAsnLeuValProSerAsnTrpGlnPheGlyGln 243
Db 667 AGCGATGGCCAAACCAATTGTCTCTTAACAAGTTGCTAAGCAGCGCTGTCTTTCGGCCAG 726
QY 244 ThrTyrgLuglyProGln 249
Db 727 ACCTTCAACAGGTGCGCAG 744

RESULT 5

US-10-409-701-8
; Sequence 8, Application US/10409701
; Publication No. US20030221224A1
; GENERAL INFORMATION:
; APPLICANT: Zinselmeier, Chris
; APPLICANT: Helentjaris, Timothy G.
; TITLE OF INVENTION: Enhanced Silk Exsersion Under Stress
; FILE REFERENCE: 1421
; CURRENT APPLICATION NUMBER: US/10/409,701
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,796
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ. ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(759)
US-10-409-701-8

Alignment Scores:

Pred. No.: 2.19e-118 Length: 759
Score: 1027.00 Matches: 177
Percent Similarity: 88.99% Conservative: 25
Best Local Similarity: 77.97% Mismatches: 25
Query Match: 73.67% Indels: 0
DB: 13 Gaps: 0

US-09-383-579c-10 (1-250) x US-10-409-701-8 (1-759)

QY 24 AspTyrGlyGlyTyrGlnSerGlyHisAlaThrPheTyrGlyGlyGlyAspAlaSerGly 43
Db 79 GACTACGGCTCGTGGCAGAGCGCCACGCCACGTTCTACGGCGGCGGCGACGCGTCTGGC 138

QY 44 ThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThr 63
Db 139 ACGATGGCGCGCGGTGCGGCTACGGGAACATGTACAGACGGGGTACGGACCAACAG 198
QY 64 ValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGluMet 83
Db 199 GCGGCGCTGAGCAGCGCGCTGTTCACGACGCGCGCGCTGCGGGTCTGTACAGCTG 258
QY 84 ThrCysThrAsnAspProLysTrpCysLeuProGlyThrIleArgValThrAlaThrAsn 103
Db 259 CGCTGCGACAAACAACGGGCGAGTCGTGCTGCCGGGCAACATCACGGCCACCAAC 318
QY 104 PheCysProProAsnPhaAlaLeuProAsnAsnGlyGlyTrpCysAsnProProLeu 123
Db 319 TTTCTGCCGCCCAACTACGGCTCTCCCAAGCAGACGGCGGCTGTGTCAACCCGCGGC 378
QY 124 GlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTrpArgAlaGlyIle 143
Db 379 CCGCACTTCGACATGGCCCAAGCCGCTTCTTCCAGATCGCGCAGTACCGCGCGCATC 438
QY 144 ValProValSerPheArgArgValProCysMetLysGlyGlyValArgPheThrIle 163
Db 439 GTGCCCTCGCTTACAGAGAGGTCCTGCTGTAAGAAAGGCGGGATCAGTTCCACATC 498
QY 164 AsnGlyHisSerTrpPheAsnLeuValLeuIleThrAsnValGlyGlyAlaGlyAspVal 183
Db 499 AACGGCACTCTTACTTCAACCTGTGTGTGACCAACGTGGCGCGCGCGGGAGCTG 558
QY 184 HisSerValSerIleLysGlySerArgTrpGlyTrpGlnSerMetSerArgAsnTrpGly 203
Db 559 CAGTCCGTGTCTCATCAAGGCTCTCCAGCAACGGGTGGCAAGCCATGTCCGCACTGGGCG 618
QY 204 GlnAsnTrpGlnSerAsnAsnTrpLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeu 223
Db 619 CAGAACTGGCAGAGCACTCGCTCTTCCAGCGGCCAGACCTGTCTTCCAGGTACCGCC 678
QY 224 SerAspGlyArgThrLeuThrAlaTrpAsnLeuValProSerAsnTrpGlnPheGlyGln 243
Db 679 AGCGACGGCGCGACCGTTCACCAAGCGCGCTCGCGGGGCTGGCAGTTGGGCGAG 738
QY 244 ThrTyrgLuglyProGlnPhe 250
Db 739 ACCTTCAGAGCGGCCCAAGTTC 759

RESULT 6

US-09-938-842A-1069
; Sequence 1069, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ. ID NOS: 5379
; SEQ ID NO 1069
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1069

Alignment Scores:

US-09-938-842A-1069

RESULT 8

US-09-938-842A-842
 ; Sequence 842, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938, 842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227, 866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264, 647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300, 111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 842
 ; LENGTH: 774
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-842

Alignment Scores:

Pred. No.:	2.23e-107	Length:	774
Score:	939.00	Matches:	161
Percent Similarity:	83.70%	Conservative:	29
Best Local Similarity:	70.93%	Mismatches:	35
Query Match:	67.36%	Indels:	2
DB:	10	Gaps:	1

US-09-383-579c-10 (1-250) x US-09-938-842A-842 (1-774)

QY 26 GYGLYTRPGLNserGlyHisAlaThrPheTyrglyGlyAspAlaSerGlyThrMet 45
 |||||:::|||||
 Db 85 GGTGGTTGGAACTGCTCAGCCACTTCTACGGTCTGTGATGCTTCTGGAACAATG 144
 |||||:::|||||
 QY 46 GYGLYAlaCySgLYTyrglyAsnLeuTyrseryGlyTyrglyThrAsnThrValAla 65
 |||||:::|||||
 Db 145 GGAGAGCTGTGGTATGTGTACTTATACAGCCAGGCTATGTGTAACACGCGGCT 204
 |||||:::|||||
 QY 66 LeuSerThrAlaLeuPheAsnAsnGlyLeuSerCySgLYAlaCyPheGluMetThrCys 85
 |||||:::|||||
 Db 205 TTAAGCACGGCTGTGTTCAACAATGTTTAACTGTGTGCTTGTGTTGAGCTCAAAATGT 264
 |||||:::|||||
 QY 86 ThrAsnAspProLYsTrpCySLeuProGly-----ThrIleArgValThrAlaThrAsn 103
 ::::|:::|||||
 Db 265 GCTAGTATCCAAATGCGTCCATTGCTAGTCCCTTCAATCTTCATCACTGCGACTAAT 324
 ::::|:::|||||
 QY 104 PheCySProProAsnDheAlaLeuProAsnAsnGlyGlyTyrcyAsnProProLeu 123
 |||||:::|||||
 Db 325 TTCTGCTCCGAACCTTGTCTCAGCCTAGTACAAATGCTGTGTTAACTCCTCTAGA 384
 |||||:::|||||
 QY 124 GlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrglyAlaGlyVal 143
 |||||:::|||||
 Db 385 CCTCACTTGTATCTGTATGCTATGCTTCTCAAGATCGCTGAGATCGTCCGGAATC 444
 |||||:::|||||
 QY 144 ValProValSerPheArgValProCySmetLYsGlyGlyValArgPheThrIle 163
 |||||:::|||||
 Db 445 GTCCCGCTCTTCCGCGAGTGCATGCCGGAAGAGAGGAATAGGTTACACATC 504
 |||||:::|||||
 QY 164 AsnGlyHisSerTyrcyAsnLeuValIleThrAsnValGlyGlyAlaGlyAspVal 183
 |||||:::|||||
 Db 505 AACGGTTCCGTTATTAACTGTGTTCTAGTCACTAACGTGCGTGGCGCCGGAACATA 564
 |||||:::|||||
 QY 184 HisSerValSerIleLYsGlySerArgThrGlyTyrcySerMetSerArgAsnTrpGly 203
 ::::|:::|||||
 Db 565 GTGGGCTAGTGTGAAGAACACATTACTTGTGATGACCATGATGATGATGATGATGATG 624
 ::::|:::|||||

RESULT 9

US-09-770-445-491/c
 ; Sequence 491, Application US/09770445
 ; Patent No. US20020023281A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gorlach, Jorn
 ; APPLICANT: An, Yong-Qiang
 ; APPLICANT: Hamilton, Carol M.
 ; APPLICANT: Price, Jennifer L.
 ; APPLICANT: Raines, Tracy M.
 ; APPLICANT: Yu, Yang
 ; APPLICANT: Rameaka, Joshua G.
 ; APPLICANT: Page, Amy
 ; APPLICANT: Matthew, Abraham V.
 ; APPLICANT: Ledford, Brooke L.
 ; APPLICANT: Woessner, Jeffrey P.
 ; APPLICANT: Haas, William David
 ; APPLICANT: Garcia, Carlos A.
 ; APPLICANT: Kricker, Maja
 ; APPLICANT: Slader, Ted
 ; APPLICANT: Davis, Keith R.
 ; APPLICANT: Allen, Keith
 ; APPLICANT: Hoffman, Neil
 ; APPLICANT: Hurban, Patrick
 ; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
 ; FILE REFERENCE: 2023US (PARA-012PRV)
 ; CURRENT APPLICATION NUMBER: US/09/770, 445
 ; PRIOR FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: US 60/178, 472
 ; NUMBER OF SEQ ID NOS: 999
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 491
 ; LENGTH: 893
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(893)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-770-445-491

Alignment Scores:

Pred. No.:	3.67e-107	Length:	893
Score:	938.00	Matches:	161
Percent Similarity:	83.70%	Conservative:	29
Best Local Similarity:	70.93%	Mismatches:	35
Query Match:	67.29%	Indels:	2
DB:	9	Gaps:	1

US-09-383-579c-10 (1-250) x US-09-770-445-491 (1-893)

QY 26 GYGLYTRPGLNserGlyHisAlaThrPheTyrglyGlyGlyAspAlaSerGlyThrMet 45
 |||||:::|||||
 Db 774 GGTGGTTGGAACTGCTCAGCCACTTCTACGGTGTGCTGTGATGCTTCTGGAACAATG 715
 |||||:::|||||
 QY 46 GYGLYAlaCySgLYTyrglyAsnLeuTyrseryGlyTyrglyThrAsnThrValAla 65
 |||||:::|||||
 Db 714 GGAGAGCTGTGGTATGTGTACTTATACAGCCAGGCTATGTGTAACACGCGGCT 655
 |||||:::|||||

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QY      66 LeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGluMetThrCys 85
Db      654 TTAAGCACGGCTGTTCAACAATGTTTAGCTGTGTGCTGTTTGTAGCTCAATGT 595

QY      86 ThrAsnAspProLysTrpCysLeuProGly-----ThrIleArgValThrAlaThrAsn 103
Db      594 GCTAGTGCATCAAAATGTTGTCATTCCTGATGCTTCAATCTTCATCAGTCACTGCACTAAT 535

QY      104 PheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTrpCysAsnProProLeu 123
Db      534 TTCTGTCTCCGAACTTGTCTCAGCCTAGTACAAATGTTGTTGTTGTAACCTCCTAGA 475

QY      124 GluHisPheAspMetAlaGluProAlaPheLeuGluIleAlaGlnTyrArgAlaGlyIle 143
Db      474 CCTCACTTGTATCTGTATGCTATGCTATGTTCTCAAGATCGCTGATATCGTCCGGAATC 415

QY      144 ValProValSerPheArgArgValProCysMetLysGlyGlyValArgPheThrIle 163
Db      414 GTCCCCGCTCTTCCCGCCGAGTCCATGCGGAAAGAGAGAGAAATAAGTTCACAATC 355

QY      164 AsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyGlyAlaGlyAspVal 183
Db      354 AACGGTTTCCGTTATTTTAACGTGTTCTAGTCACTAACGTNNNGGCCGCCGAAACATA 295

QY      184 HisSerValSerIleLysGlySerArgThrGlyTyrGlnSerMetSerArgAsnTrpGly 203
Db      294 GTCCGGCTAGGTGTGAAGAAGACATACTTCCGTGGATGACCATGAGTCGTAACTGGGGA 235

QY      204 GluAsnTrpGlnSerAsnAsnTrpLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeu 223
Db      234 CAAAACTGGCAATCTAATCTAGTTTGGTGTGTCAGTCACTTTCTTTAGAGTCACAAGC 175

QY      224 SerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGlnPheGlyGln 243
Db      174 AGTGACCGTAGAAGCTCGACGTCGTGAACATTGCTCCGCCAAATTGGAAGTTTGTCTAG 115

QY      244 ThrTyrGluGlyProGlnPhe 250
Db      114 ACTTTCATGGGAAAGAACTTC 94

```

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RESULT 10
US-09-938-842A-1046
; Sequence 1046, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1046
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1046

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Alignment Scores:
Pred. No.: 7.98e-95      Length: 768
Score: 838.50           Matches: 152
Percent Similarity: 76.83%      Conservative: 37
Best Local Similarity: 61.79%      Mismatches: 50
Query Match: 60.15%           Indels: 7

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DB:      10      Gaps:      4
US-09-383-579c-10 (1-250) x US-09-938-842A-1046 (1-768)

QY      8 PheSerSerLeuPheLeuLeuProPhe-----PhePheValPheThrPheAlaAsp 24
Db      13 TTCTCTATATGTCGCAATGATCTTCTCCAAATATGTTCTTCATGAAGATCAGTCACT 72

QY      25 TyrGlyGlyTyrGlnSerGlyHisAlaThrPheTyrGlyGlyAlaAspAlaSerGlyThr 44
Db      73 TCTGCTGTTGTTGTCGAAGCTCATCGACCTTTTATGCGGGAAGTATGCTCTGTGACA 132

QY      45 MetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThrVal 64
Db      133 ATGGGTGAGCTGTGTGTTATGGAACCTTATACACAGACGGCTTACAAGACAAACACCGCG 192

QY      65 AlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGluMetThr 84
Db      193 GCGTTAAGCACGGCCCTGTTCAACGACGGCAAGTCATGCGGTGATGTTACCAATCTTG 252

QY      85 Cys-----ThrAsnAspProLysTrpCysLeuProGly---ThrIleArgValThrAla 101
Db      253 TGTGATGCACCAAGTACCAACAATGTTGTTTAAAGGCAAAATCAATCACTATTCACAGCT 312

QY      102 ThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTyrCysAsnPro 121
Db      313 ACAAACTTCTGTCCACCGAACTTGTCTCAGGCAAGCAGCAATGAGGTTGTGCAACCCA 372

QY      122 ProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAla 141
Db      373 CCGAGACCTCATTTGACATGCTCAGCCTGCGTTTCTCACCATCGCTAAGTACAAAGCT 432

QY      142 GlyIleValProValSerPheArgArgValProCysMetLysGlyGlyValArgPhe 161
Db      433 GGAATCGTCCCATTTCTTTACAAAAAGTTGATGTAGAAGACGGAGGATGAGATT 492

QY      162 ThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyAlaGly 181
Db      493 ACAATTAACGGTAGAAACTTATTCGAGCTGTCTCATCTCAAAACGTAGACGAGGGGGT 552

QY      182 AspValHisSerValSerIleLysGlySerArgThrGly---TrpGlnSerMetSerArg 200
Db      553 GAGATCTCTTAAAGTTTGGATCAAAAGATCTTAAAGACAAATGGGAGACATGTCAGA 612

QY      201 AsnTrpGlyGlnAsnTrpGlnSerAsnAsnTrpLeuAsnGlyGlnGlyLeuSerPheGln 220
Db      613 AATTGGGGAAGCTAATTATCAGAGTAATACTTAACCTTAATGTCATCTTCTTTCAAA 672

QY      221 ValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGln 240
Db      673 GTTCAACTTAAGTATGAGTATCAAGACGCTCTCAACGTTGTTCTTCGAATTGGCGG 732

QY      241 PheGlyGlnThrTyrGlu 246
Db      733 TTTGTCAAGACTTCAAG 750

RESULT 11
US-09-878-574-3973
; Sequence 3973, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Ia Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3973

```

; LENGTH: 410
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-003-Q1-B1-D9
US-09-878-574-3973

Alignment Scores:

Pred. No.:	6.44e-75	Length:	410
Score:	676.00	Matches:	120
Percent Similarity:	96.30%	Conservative:	10
Best Local Similarity:	88.89%	Mismatches:	5
Query Match:	48.49%	Indels:	0
DB:	10	Gaps:	0

US-09-383-579C-10 (1-250) x US-09-878-574-3973 (1-410)

QY 113 AsnAsnAnglYgLYTrpCyAsnProLeuGlnHisPheAspMetAlaGluProAla 132
|||||
Db 5 AACACAAATGGTGGCTGCAACCCCTTGGCAACCTTGATCTTGCTGAGCTGCT 64

QY 133 PheLeuGlnIleAlaGlnTyrArgAlaGlyIleValProValSerPheArgValPro 152
|||||
Db 65 TTCTGCAAAATGCTCAATACAAAGCTGGAATTGTCAGTTCTTCCAGAGAGTCTCC 124

QY 153 CysMetIleYsGlyGlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeuVal 172
|||||
Db 125 TGTGTGAAGAAAGAGGATCAGGTTCACCATCAATGTCCTTACTTCAACTTGCTT 184

QY 173 LeuIleThrAsnValGlyGlyAlaGlyAspValHisSerValSerIleYsGlySerArg 192
|||||
Db 185 CTCAATCAAAATGTTGGTGGAGCTGGAGATGTTCAATCTGTGTCATCAAAAGGTCTAGA 244

QY 193 ThrGlyTrpGlnSerMetSerArgAsnTrpGlyGlnAsnTrpGlnSerAsnTrpLeu 212
|||||
Db 245 ACTGGGTGGCAAAACCAATGCTAGAACTGGGGCAGAAATTGTAAGCAACTCTACTG 304

QY 213 AsnGlyGlnGlyLeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTyr 232
|||||
Db 305 AATGGCCAAAGCCTCTCTTTTTCAGGTCACTACAGTATGGCAGACTCTCCTAGCAAC 364

QY 233 AsnLeuValProSerAsnTrpGlnPheGlyGlnThrTyrGluGly 247
|||||
Db 365 AACATTGTGCTGCTAAGTCACTGCAATTGGACAAACATTGGAAGGG 409

RESULT 12

US-09-878-574-62
; Sequence 62, Application US/09878574
; Patent No. US20020110548A1

GENERAL INFORMATION:

; APPLICANT: Byrum, Joseph R.
; APPLICANT: Ia Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; NUMBER OF SEQ ID NOS: 15775

SEQ ID NO 62

LENGTH: 391

TYPE: DNA

ORGANISM: Glycine max

FEATURE:

NAME/KEY: unsure

LOCATION: (1)..(391)

OTHER INFORMATION: unsure at all n locations

OTHER INFORMATION: Clone ID: LIB3028-056-Q1-B1-E10

US-09-878-574-62

Alignment Scores:

Pred. No.: 7.99e-71

Length: 391

Score:	643.00	Matches:	112
Percent Similarity:	96.15%	Conservative:	13
Best Local Similarity:	86.15%	Mismatches:	5
Query Match:	46.13%	Indels:	0
DB:	10	Gaps:	0

US-09-383-579C-10 (1-250) x US-09-878-574-62 (1-391)

QY 116 GlyGlyTrpCyAsnProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGln 135
|||||
Db 1 GGTGGTGGTGAACCCCTCTTGGCAACACTTGATATGCTGAACCTGCTTCTTCAA 60

QY 136 IleAlaGlnTyrArgAlaGlyIleValProValSerPheArgValProCysMetLys 155
|||||
Db 61 ATTGCTGAATATAGACTGGAATTGTGCTGCTTCAAGAGGCTTCTTGTGAAA 120

QY 156 LysGlyGlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThr 175
|||||
Db 121 AAGGAGGAATAGGTTCAACATCAATGCGCACCTTACTTCACTAGTTTGTATCACC 180

QY 176 AsnValGlyGlyAlaGlyAspValHisSerValSerIleYsGlySerArgThrGlyTrp 195
|||||
Db 181 AATGTGGCTGAGCTGTGATGTAATTCAGTGTCCATTAAAGGCTCCAAACCTGGGTGG 240

QY 196 GlnSerMetSerArgAsnTrpGlyGlnAsnTrpGlnSerAsnTrpLeuAsnGlyGln 215
|||||
Db 241 CAGCCCATGTCAAGAACTGGGGCAAACTGGCAGAGCAACTCATACCTCAATGACAA 300

QY 216 GlyLeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuVal 235
|||||
Db 301 TCNCTCTCTTTCAAGTCAACCACTGATGCGCAGAACTGTGACAACTTCAATGTGCA 360

QY 236 ProSerAsnTrpGlnPheGlyGlnThrTyr 245
|||||
Db 361 CCAGCCAAATTGGCAATTGGCCAGACCTTC 390

RESULT 13

US-09-770-791-430
; Sequence 430, Application US/09770791
; Patent No. US20020062014A1

GENERAL INFORMATION:

; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2029 (PARA-018PRV)
; CURRENT APPLICATION NUMBER: US/09/770,791
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,480
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastsEQ for Windows Version 4.0
; SEQ ID NO 430

LENGTH: 366

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-770-791-430

Alignment Scores:

Pred. No.:	9.54e-54	Length:	366
Score:	506.00	Matches:	85
Percent Similarity:	87.27%	Conservative:	11
Best Local Similarity:	77.27%	Mismatches:	12
Query Match:	36.30%	Indels:	2
DB:	9	Gaps:	1

US-09-383-579C-10 (1-250) x US-09-770-791-430 (1-366)

QY 26 GlyGlyTTrpGlnSerGlyHisAlaThrPheTyrGlyGlyAlaSerGlyThrMet 45

DB 36 GGACCGTGGCAGATGCACACGCCACTTCTACGGTGCAGTGCAGCCCTCCGGCACAATG 95

QY 46 GlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThrValAla 65

DB 96 GCGCGCGGTGGTGGTACGGGAATTGTACAGCCAGGATACGGTGTGAACACGGCGCGG 155

QY 66 LeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGlnMetThrCys 85

DB 156 TTGAGCACTGCTTGTTCACACAGGATTTCAGCTGTGCTGCTTTTGAGATTAAAGTGT 215

QY 86 ThrAsnAsnProLysTyrCysLeuProGly-----ThrIleArgValThrAlaThrAsn 103

DB 216 ACTGATGATCCGAGATGCTGTCTCCGGGAATCCATCTATTCTGTGACGGCGCAGAAC 275

QY 104 PheCysProProAsnPheAlaLeuProAsnAsnGlyGlyTyrCysAsnProProLeu 123

DB 276 TTTTGTCCGCCGAATTTGTCTCAGCCGAGTGCAGCAGGAGGTGTGCAATCCGCCGCCG 335

QY 124 GlnHisPheAspMetAlaGluProAlaPhe 133

DB 336 GAGCATTTGATCTCGCCATGCTATGTTC 365

RESULT 14

US-09-878-574-3468

; Sequence 3468, Application US/09878574

; Patent No. US20020110548A1

; GENERAL INFORMATION:

; APPLICANT: Byrum, Joseph R.

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Thompson, Michael D.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(15401)B

; CURRENT APPLICATION NUMBER: US/09/878,574

; PRIOR FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: 09/333,535

; PRIOR FILING DATE: 1999-06-14

; NUMBER OF SEQ ID NOS: 15775

; SEQ ID NO 3468

; LENGTH: 373

; TYPE: DNA

; ORGANISM: Glycine max

; OTHER INFORMATION: Clone ID: LIB3028-010-Q1-B1-E9

US-09-878-574-3468

Alignment Scores:

Pred. No.:	6.36e-52	Length:	373
Score:	491.50	Matches:	85
Percent Similarity:	78.40%	Conservative:	13
Best Local Similarity:	68.00%	Mismatches:	16
Query Match:	35.26%	Indels:	11
DB:	10	Gaps:	2

US-09-383-579C-10 (1-250) x US-09-878-574-3468 (1-373)

QY 12 PheLeuLeuProPhePhePheValPheThrPheAla-----AspTyrGlyGlyTyr 28

DB 21 TTTCTTCTGGACTTTTCTACATGATCTCACATGTCAAGGGTATGTTTGGAGGTTGG 80

QY 29 GlnSerGlyHisAlaThrPheTyrGlyGlyAlaSerGlyThrMetGlyGlyAla 48

DB 81 ACCAATGCACATGCCACCTTCTATGAGGGGTGATGCTTCTGGACAATGGGTGGGCT 140

QY 49 CysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThrValAlaLeuSerThr 68

DB 141 TGTGTATGGAATCTGTATAGCCAGGTTATGGAAGTATACACAGCACTGAGCACT 200

QY 69 AlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGlnMetThrCysThrAsnAsp 88

DB 201 GCACGTGTTCACAAATGGCTTAAGCTGTGGTCATGCTTCAATAATTAATGCGCAATGAC 260

QY 89 ProLysTyrCysLeuProGlyThrIleArgValThrAlaThrAsnPheCysProProAsn 108

DB 261 CCACATGTGCTCTCCCTGCTCCATCATAGTCACCTGCCACAATTCTGTCCACCT--- 317

QY 109 PheAlaLeuProAsnAsnGlyGlyTyrCysAsnProProLeuGlnHisPheAspMet 128

DB 318 -----GGTGTGTGTGTGACCCCTCCCAATCACCACTTTGATCCT 356

QY 129 AlaGluProAlaPhe 133

DB 357 TCCCAACTGCTTTC 371

RESULT 15

US-09-878-574-1206

; Sequence 1206, Application US/09878574

; Patent No. US20020110548A1

; GENERAL INFORMATION:

; APPLICANT: Byrum, Joseph R.

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Thompson, Michael D.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(15401)B

; CURRENT APPLICATION NUMBER: US/09/878,574

; PRIOR FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: 09/333,535

; PRIOR FILING DATE: 1999-06-14

; NUMBER OF SEQ ID NOS: 15775

; SEQ ID NO 1206

; LENGTH: 391

; TYPE: DNA

; ORGANISM: Glycine max

; OTHER INFORMATION: Clone ID: LIB3028-040-Q1-B1-G6

US-09-878-574-1206

Alignment Scores:

Pred. No.:	3.79e-39	Length:	391
Score:	389.50	Matches:	75
Percent Similarity:	78.70%	Conservative:	10
Best Local Similarity:	69.44%	Mismatches:	16
Query Match:	27.94%	Indels:	7
DB:	10	Gaps:	3

US-09-383-579C-10 (1-250) x US-09-878-574-1206 (1-391)

QY 1 MetAlaPheSerTyrSerProPheSer---SerLeuPheLeuLeuProPhePheVal 19

DB 67 CTTAGATGGCACACACAGGAATTTCCATTGCCCTAGTACTCTCATTTGTTCTTTGTC 126

QY 20 PheThr-----PheAlaAspTyr--GlyGlyTyrGlnSerGlyHisAla 33

DB 127 AACACGAACCTCCAAGTGCACAGGCTGACTATAGTGTGTTGGCAGAGTCTCATGCC 186

QY 34 ThrPheTyrGlyGlyGlyAspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsn 53

DB 187 ACTTCTATGTGTGGGTGATGCTTCTGACCAATGGGTGAGCATGTGGGTATGGAAT 246

QY 54 LeuTyrSerGlnGlyTyrGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsn 73

DB 247 TTGTATAGCCAGGATATGGAAGTACACTGTGCTTAAAGCACTGCTTTGTTCAACAAT 306

Qy	74	GlyLeuSerCysGlyAlaCysPheGluMetThrCysThrAsnAspProLysTrpCysLeu	93
Db	307	GGCTTAAGCTGATGATCTTGTCTATGAATGAGATGTGATGATGACCAAGATGGTCAAA	366
Qy	94	ProGlyThrIleArgValThrAla	101
Db	367	CCTGGCTCTATTACCGTCACTGCT	390

Search completed: December 19, 2003, 02:03:22
 Job time : 296 secs

C/Species: Pinus taeda (loblolly pine)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C/Accession: T09821
R/Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
submitted to the EMBL Data Library, July 1996
A/Description: Expansins are conserved in conifers and expressed in response to exogenous
A/Reference number: Z16866
A/Accession: T09821
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-232 <HUT>
A/Cross-references: EMBL:U64891; NID:g1778100; PID:g1778101
A/Experimental source: clone pTexp3
C/Superfamily: expansin

Query Match	78.3%;	Score 1092;	DB 2;	Length 232;
Best Local Similarity	82.7%;	Pred. No. 3.7e-85;		
Matches 186;	Conservative 22;	Mismatches 17;	Indels 0;	Gaps 0;

```
QY      25 YGGMQSGHATFYGGGDASGTMGACGYGNLYSQGYGTNTVALSTALFNNGISCGACPEMT   84
       |||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      7 YGGMESAHATFYGGSDASGTMGACGYGNLYSQGYGTNTAALSTALFNDGISCGACYENR   66
```

```
QY      85 CTNDPKMCLPGTIRVTATNFCRPNFALPNNNGWCNPLOHFDMAEPALOIAQRAGIV 144  
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db     67 CNDPEQMCLPGTVITVATA TNFCRPNNALENDNGGCWCPLOHFDMAEPAFLKAKYRGIV 120
```

```
Qy      145 PVSEFRRVPCKKGAVREFTINGHSYFNLVLTINVGAGDVHVSISKSRRTGQMSRNMGQ 204  
        |: : |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||  
Db     127 PILYTRVPCLRKRGIRFTVNGHSYFNVLTLTNVGAGDVAHAVISIKGRSCGWPMRSRMGQ 186
```

```
QY      205  NMOSSNYLNGGGSFQVTLSDGRLLTAYNLVPSNMQFGQTYEGPQ 249
        ||||:||||| ||||| ||||| : : ||||| ||||| : |||
Db      187  NMOSSNYLNGGGSLSFQVTTSDGRIVVSNNAVPSNMQFGQTFEGSQ 231
```

RESULT 3
T09818

expansin (clone pTexp2) - loblolly pine (fragment)
C/Species: Pinus taeda (loblolly pine)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C/Accession: T09818
R/Hutchinson, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
submitted to the EMBL Data Library, July 1996
A/Description: Expansins are conserved in conifers and expressed in response to exogenous
A/Reference number: Z16866
A/Accession: T09818
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-232 <HUT>
A/Cross-references: EMBL:U64890; NID:g1778098; PID:g1778099
A/Experimental source: clone pTexp2; hypocotyl
C/Superfamily: expansin

Query Match	78.0%;	Score 1087;	DB 2;	Length 232;
Best Local Similarity	82.2%;	Pred. No. 9.9e-85;		
Matches 185; Conservative	22;	Mismatches 18;	Indels 0;	Gaps 0.

QY 25 YGMSQGHAIFYGGDASGTMGACGYGNLYSQGYTNTVALSTALFNNGHSCGACFEHT 84
|||::||||| ||||| ||||| ||||| : ||||| ::
Dd 7 YGWESAHATFYGGSDASGTMGACGYGNLYSQGYTNTAAISTALFNDIGLSCGACYEMR 66

[illegible]

```
QY      145 PVSFRRPVCMKKGVRFTINGHSYFNLVLTITNVGAGDVHSYSIKGSRITGQMSMRNQ 204
      127 PLYTRVPCLRKGGIRFTVNGHSYFNLVLTITNVGAGDVHSAVSIKGSMSGQDMSRNRNQ 186
Db
```

```
QY      205  NMOSNNYLNQGLSFQVTLSDGRLLAYNLVLPSPNMQFGQTYEGPQ 249
        ||||:||||| ||||| ||||| : : ||||| ||||| |||||
Db      187  NMOSNSYLNQGLSFQVTTSDGRITVSNNAVAPSPNMQFGQTFEGSQ 231
```

RESULT 4
T09826
expansin (clone pTexp5) - loblolly pine (fragment)
C/Species: Pinus taeda (loblolly pine)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C/Accession: T09826
R/Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
submitted to the EMBL Data Library, July 1996
A/Description: Expansins are conserved in conifers and expressed in response to exogenous
A/Reference number: Z16866
A/Accession: T09826
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-232 <HUT>
A/Cross-references: EMBL:U64893; NID:g1778104; PID:g1778105
A/Experimental source: clone pTexp5
C/Superfamily: expansin

Query Match	77.8%	Score 1085;	DB 2;	Length 232;
Best Local Similarity	82.2%	Pred. No. 1.5e-84;		
Matches 185; Conservative	23;	Mismatches 17;	Indels 0;	Gaps 0;

```
Oy      25 YGWSQGHATFYGGGDASGTWGCACGYGNLYSQYGTNTVALSTALFNNGISCGACFEEMT   84  
       ||| : | ||||| | ||||| | ||||| | ||||| : ||||| : ||  
Db     7 YGWESAHATFYGGS DASGTWGCACGYGNLYSQYGTNTAALSTALFNNDGISCGACYE M Q    66
```

[illegible]

```
Qy      145 PVSERRRVPCKKGGVRFITNGHSYENLVLTINVGAGDVHVSISIKGSRFGWQSMRSRWGQ 204
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      127 PLIYTRVPCLRKKGIRFTVNGHSYENLVLTINVGAGDVNAVISIKGSRSQWQPMSRWNGQ 186
```

```
Qy      205  NMQSNMYLNGQGLSFQVTLSDGRITLAYNLVPSNMQFGQTYEGPO 249
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      187  NMQSNXYLNGQGLSFQVTTSDGRITVSNNAVPSNMQFGQTFEGSQ 231
```

RESULT 5
F84831

probable expansin [imported] - *Arabidopsis thaliana*
C/Species: *Arabidopsis thaliana* (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C/Accession: F84831
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A/Reference number: A84420; MUID:20083487; PMID:10617197

```

;Status: preliminary
;Molecule type: DNA
;Residues: 1-253 <STO>

```

C;Genetics: [1](#) [2](#) [3](#) [4](#) [5](#) [6](#) [7](#) [8](#) [9](#) [10](#) [11](#) [12](#) [13](#) [14](#) [15](#) [16](#) [17](#) [18](#) [19](#) [20](#) [21](#) [22](#) [23](#) [24](#) [25](#) [26](#) [27](#) [28](#) [29](#) [30](#) [31](#) [32](#) [33](#) [34](#) [35](#) [36](#) [37](#) [38](#) [39](#) [40](#) [41](#) [42](#) [43](#) [44](#) [45](#) [46](#) [47](#) [48](#) [49](#) [50](#) [51](#) [52](#) [53](#) [54](#) [55](#) [56](#) [57](#) [58](#) [59](#) [60](#) [61](#) [62](#) [63](#) [64](#) [65](#) [66](#) [67](#) [68](#) [69](#) [70](#) [71](#) [72](#) [73](#) [74](#) [75](#) [76](#) [77](#) [78](#) [79](#) [80](#) [81](#) [82](#) [83](#) [84](#) [85](#) [86](#) [87](#) [88](#) [89](#) [90](#) [91](#) [92](#) [93](#) [94](#) [95](#) [96](#) [97](#) [98](#) [99](#) [100](#) [101](#) [102](#) [103](#) [104](#) [105](#) [106](#) [107](#) [108](#) [109](#) [110](#) [111](#) [112](#) [113](#) [114](#) [115](#) [116](#) [117](#) [118](#) [119](#) [120](#) [121](#) [122](#) [123](#) [124](#) [125](#) [126](#) [127](#) [128](#) [129](#) [130](#) [131](#) [132](#) [133](#) [134](#) [135](#) [136](#) [137](#) [138](#) [139](#) [140](#) [141](#) [142](#) [143](#) [144](#) [145](#) [146](#) [147](#) [148](#) [149](#) [150](#) [151](#) [152](#) [153](#) [154](#) [155](#) [156](#) [157](#) [158](#) [159](#) [160](#) [161](#) [162](#) [163](#) [164](#) [165](#) [166](#) [167](#) [168](#) [169](#) [170](#) [171](#) [172](#) [173](#) [174](#) [175](#) [176](#) [177](#) [178](#) [179](#) [180](#) [181](#) [182](#) [183](#) [184](#) [185](#) [186](#) [187](#) [188](#) [189](#) [190](#) [191](#) [192](#) [193](#) [194](#) [195](#) [196](#) [197](#) [198](#) [199](#) [200](#) [201](#) [202](#) [203](#) [204](#) [205](#) [206](#) [207](#) [208](#) [209](#) [210](#) [211](#) [212](#) [213](#) [214](#) [215](#) [216](#) [217](#) [218](#) [219](#) [220](#) [221](#) [222](#) [223](#) [224](#) [225](#) [226](#) [227](#) [228](#) [229](#) [230](#) [231](#) [232](#) [233](#) [234](#) [235](#) [236](#) [237](#) [238](#) [239](#) [240](#) [241](#) [242](#) [243](#) [244](#) [245](#) [246](#) [247](#) [248](#) [249](#) [250](#) [251](#) [252](#) [253](#) [254](#) [255](#) [256](#) [257](#) [258](#) [259](#) [260](#) [261](#) [262](#) [263](#) [264](#) [265](#) [266](#) [267](#) [268](#) [269](#) [270](#) [271](#) [272](#) [273](#) [274](#) [275](#) [276](#) [277](#) [278](#) [279](#) [280](#) [281](#) [282](#) [283](#) [284](#) [285](#) [286](#) [287](#) [288](#) [289](#) [290](#) [291](#) [292](#) [293](#) [294](#) [295](#) [296](#) [297](#) [298](#) [299](#) [300](#) [301](#) [302](#) [303](#) [304](#) [305](#) [306](#) [307](#) [308](#) [309](#) [310](#) [311](#) [312](#) [313](#) [314](#) [315](#) [316](#) [317](#) [318](#) [319](#) [320](#) [321](#) [322](#) [323](#) [324](#) [325](#) [326](#) [327](#) [328](#) [329](#) [330](#) [331](#) [332](#) [333](#) [334](#) [335](#) [336](#) [337](#) [338](#) [339](#) [340](#) [341](#) [342](#) [343](#) [344](#) [345](#) [346](#) [347](#) [348](#) [349](#) [350](#) [351](#) [352](#) [353](#) [354](#) [355](#) [356](#) [357](#) [358](#) [359](#) [360](#) [361](#) [362](#) [363](#) [364](#) [365](#) [366](#) [367](#) [368](#) [369](#) [370](#) [371](#) [372](#) [373](#) [374](#) [375](#) [376](#) [377](#) [378](#) [379](#) [380](#) [381](#) [382](#) [383](#) [384](#) [385](#) [386](#) [387](#) [388](#) [389](#) [390](#) [391](#) [392](#) [393](#) [394](#) [395](#) [396](#) [397](#) [398](#) [399](#) [400](#) [401](#) [402](#) [403](#) [404](#) [405](#) [406](#) [407](#) [408](#) [409](#) [410](#) [411](#) [412](#) [413](#) [414](#) [415](#) [416](#) [417](#) [418](#) [419](#) [420</](#)

Query Match	77.8%;	Score 1085;	DB 2;	Length 253;
Best Local Similarity	77.9%;	Pred. No. 1.6e-84;		

QY 4 SYSPFSSLELIPFFV-FTPADYGMQSGHATFYGGGDASGTMGACCGYNLYSQGYGTN 62

63 TVALSTALFNNGLSGACFEEMTCITNDBKWCCLPGTIRVYATNFCPPNFALENNNGGWCNPP 122

Db 65 TAAALSTALFNNGLTGCACYEMKCNDDPRWCIGSTITVTATNFCPPNGLSNDNGWCNP 124

Qy 123 LQHFDMAPFLQIAQYRAGIVPVSFRVRPCMKKGVRFTINGHSYFNLVLTNVGAGD 182

Db 125 LQHFDMAPFLQIAQYRAGIVPVSFRVRPCMKKGIRFTINGHSYFNLVLTNVGAGD 184

Qy 183 VHSVSIKGSRT-GWQMSRRNGQNNQNNYLNQGLSFQVTLSDGRTLTAAYNLVPSNMQF 241

Db 185 VHAIVSIKGSRTQSWQAMSRNGQNNQNNYLNQGLSFQVTLSDGRTLVSNDVAPSNMQF 244

Qy 242 GQTYEGPOF 250

Db 245 GQTYEGPOF 253

RESULT 6

T09825

expansin (clone pTexp4) - loblolly pine (fragment)

C:Species: Pinus taeda (loblolly pine)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000

C:Accession: T09825

R:Hutchinson, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.

A:Submitted to the EMBL Data Library, July 1996

A:Description: Expansins are conserved in conifers and expressed in response to exogenous

A:Reference number: Z16866

A:Accession: T09825

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-232 <HUT>

A:Cross-references: EMBL:U64892; NID:g1778102; PID:g1778103

A:Experimental source: clone pTexp4

C:Superfamily: expansin

Query Match 77.3%; Score 1077; DB 2; Length 232;

Best Local Similarity 81.3%; Pred. No. 6.9e-84;

Matches 183; Conservative 23; Mismatches 19; Indels 0; Gaps 0;

Qy 25 YGGMQSGHATFYGGDASGTMGACGYNLYSQGYGTNTVALSTALFNNGLSCGACFEMT 84

Db 7 YGGMESAHATFYGGSDASGTMGACGYNLYSQGYGTNTALSTALFNDGLSCGACYEMQ 66

Qy 85 CTNDPKWCLPRTIRVATATNFCPPNFALPNNNGWCNPPLQHFDMAPFLQIAQYRAGIV 144

Db 67 CNDPQWCLPRTITATNFCPPNFALPNDNGWCNPPLQHFDMAPFLKAKYRGIV 126

Qy 145 PVSFRVRPCMKKGVRFTINGHSYFNLVLTNVGAGDVHVSIVKGSRTGQMSRRNGQ 204

Db 127 PLYTRVPCLRKGIKIRFTVNGHSCFNLVLTNVGAGDVHVSIVKGRSGWQPMSSRRNGQ 186

Qy 205 NMQSNLYLNQGLSFQVTLSDGRTLTAAYNLVPSNMQFQTYEGPO 249

Db 187 NMQSNLYLNQGLSFQVTLSDGRTLVSNDVAPSNMQFQTYEGSQ 231

RESULT 7

T09786

expansin - upland cotton

C:Species: Gossypium hirsutum (upland cotton)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000

C:Accession: T09786

R:Orford, S.J.; Timmis, J.N.

Biochim. Biophys. Acta 1398, 342-6, 1998

A:Title: Specific expression of an expansin gene during elongation of cotton fibres.

A:Reference number: Z14468; MUID:9655931; PMID:9655931

A:Accession: T09786

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-258 <ORF>

A:Cross-references: EMBL:AF043284; NID:g2811277; PID:g2811278

A:Experimental source: cultivar Siokra 1-2

C:Genetics:

A:Gene: GHEX1

C:Function:

A:Description: involved in cell wall modification

C:Superfamily: expansin

Query Match 75.4%; Score 1051; DB 2; Length 258;

Best Local Similarity 74.3%; Pred. No. 1.2e-81;

Matches 182; Conservative 28; Mismatches 25; Indels 10; Gaps 1;

Qy 16 FFFVFTFA-----DYGMQSGHATFYGGDASGTMGACGYNLYSQGYGTNTVA 65

Db 14 FFFLFSVCNSIFLGANGDNGWQTAHATFYGGADATGTMGACGYNLYSQGYGTSTAA 73

Qy 66 LSTALFNNGLSCGACFEMTCTNDPKWCLPRTIRVATATNFCPPNFALPNNNGWCNPLOH 125

Db 74 LSTALFNNGLSCGACYELRCNNDPQWCISRTITVTATNFCPPNYALSDNGWCNPPEH 133

Qy 126 FDMAPFLQIAQYRAGIVPVSFRVRPCMKKGVRFTINGHSYFNLVLTNVGAGDVHS 185

Db 134 FDLAPFLQIAQYRAGIVPVSFRVRPCMKKGIRFTINGHSYFNLVLTNVGAGDITS 193

Qy 186 VSIKGSRTGQMSRRNGQNNQNNYLNQGLSFQVTLSDGRTLTAAYNLVPSNMQFQTY 245

Db 194 VSIKGSRTGWLPMSSRRNGQNNQNNYLNQGLSFQVTLSDGRTLTAAYNVPAWQFQTF 253

Qy 246 EGPQF 250

Db 254 EGGQF 258

RESULT 8

T03298

expansin 2 - rice

C:Species: Oryza sativa (rice)

C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000

C:Accession: T03298

R:Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Gultinan, M.J.; McQueen-Mason, S.J.; Shieh

Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995

A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, mult

A:Reference number: Z14894; MUID:96016146; PMID:7568110

A:Accession: T03298

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-251 <SHC>

A:Cross-references: EMBL:U30477; NID:g1041709; PIDN:AAB38074.1; PID:g1041710

C:Genetics:

A:Gene: EXP2

C:Function:

A:Description: induces extension (creep) in plant cell

C:Superfamily: expansin

Query Match 74.8%; Score 1043; DB 2; Length 251;

Best Local Similarity 74.6%; Pred. No. 5.7e-81;

Matches 185; Conservative 24; Mismatches 31; Indels 8; Gaps 2;

Qy 9 SSLFLPFFVFTF-----ADYGMQSGHATFYGGDASGTMGACGYNLYSQGYTN 62

Db 6 SALLLL--FSAFCFLARRAADYGSWQSAHATFYGGDASGTMGACGYNLYSTGYTN 63

Qy 63 TVALSTALFNNGLSCGACFEMTCTNDPKWCLPRTIRVATATNFCPPNFALPNNNGWCNP 122

Db 64 TAASTALFNDGAACRSCYELRCNDNGWCLPGSVTVATATNLCPNYALPNDGWCNP 123

Qy 123 LQHFDMAPFLQIAQYRAGIVPVSFRVRPCMKKGVRFTINGHSYFNLVLTNVGAGD 182

Db 124 RPHFDMAPFLQIAQYRAGIVPVSFRVRPCMKKGIRFTINGHSYFNLVLTNVAGPD 183

Qy 183 VHSVSIKGSRTGQMSRRNGQNNQNNYLNQGLSFQVTLSDGRTLTAAYNLVPSNMQF 242

Db 184 VQSVSIKGSRTGQMSRRNGQNNQNNYLNQGLSFQVAVSDGRTVTSNNVVPAGWQFX 243

Qy 243 QTYEGPOF 250

Db 244 QTYEGPOF 251

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-248 <STO>
A:Cross-references: GB:AE002093; MID:g3461833; PIDN:AAC32927.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g03090
A:Map position: 2
C:Superfamily: expansin

Query Match	73.5%;	Score 1024;	DB 2;	Length 248;
Best Local Similarity	78.1%;	Pred. No. 2.3e-79;		
Matches 175;	Conservative 23;	Mismatches 26;	Indels 0;	Gaps 0

Qy 27 GWQSGHATFYGGGDASGTMGAICYGNLYSGCYGTNTVALSTALFNNGLSCGACPFEMTCT 86
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 24 GWNVAHATFYGGSDASGTMGAICYGNLYSGCYGTNTAALSTALFNNGLSCGACFEIKCQ 83

QY 87 NDKRMCLPGTIRVATNFCPPNFALPNNNGGWCNPLOHFDMAEPFLQIAQYRAGIVPV 146
:
DB 84 SDGAMCLPGAIIVTATNFCPPNNMALPNNAAGMCNPLHHFIDLSPVFQRITAQYKAGVVP 143

```
QY      147  SFRVPCMKKGAVFTINGHSYENLVLTNVGAGDVHSVSIKGSRTQMSRNMGQNW 206
      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      144  SYRVPCMRGGRFTINGHSYENLVLTNVGAGDVHSVAVKGSRTQMQRNMGQNW 203
```

```

QY 207 QSNNTYINGGSLSFQVTLSDGRITLTAYNLVPSNMQFGQTYEGPQF 250
      ||||| ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 204 QSNNTLNGALSFKVTASDGRITVSNNTIAPASMSFGQFTTGRQF 247

```

RESULT 13

D84820

probable expansin [imported] - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C:Accession: D84820

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: D84820

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-257 <STO>

A:Cross-references: GB:AE002093; NID:g2795809; PIDN:AAB97125.1; GSPDB:GNO0139

C:Genetics:

A:Gene: At2g39700

A:Map position: 2

C:Superfamily: expansin

Query Match	71.2%;	Score 993;	DB 2;	Length 257;
Best Local Similarity	71.4%;	Pred. No. 9.9e-77;		
Matches 177;	Conservative 24;	Mismatches 37;	Indels 10;	Gaps 2.

```

Qy      13 LPPFFVFTPADY-----GGWOSGHATFYGGGDASGTMGACGYNLYSQGYGTNTV 64
      |  :  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      8 LFTTFVLFSLDARIPGIYSGGAWONAHATFYGGSDASGTMGACGYNLYSQGYGTNTA 67

```

```

QY      65 ALSTALFNNGLSCGACFEFMTCTNDPKKCLPG--TIRVATNFCPPNPALENNNGGWCNPP 122
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      68 ALSTALFNNGMSGGACFELKCANDPQCHSGSPSILITATNFCPPNLAQPSDNGGWCNPP 127

```

```
QY      123 LQHFDMAEPFLQIAQYRAGIVPVSFRRVPCMKGGVFPTINGHSYFNVLITNVGACD 1822
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      128 REHFDLAMPVFLKTAQYRAGIVPVSYRRVPCKRKGIRFTINGHRFYFNVLITNVAGAD 1877
```

```
Qy      183 VHSVSIKGSRTGWSMSRNNWGQNNSNYLNGOGLSPFYUTLSDGRTLTAYNLVPSNMWQG 242
        :|:|||||||:||:|||||||:|||||||:|||||||:|||||||:|||||||:
Db      188 IYRASVKGSRTGMNLSRNWGQNNSNAVLVGALSFYATGSDRRTSTSMNVVPSPNMWQG 247
```

QY 243 QTYEGPQF 250

Db 248 QTEVGKNF 255

RESULT 14
T47689

expansin-like protein - Arabidopsis thaliana
N:Alternate names: protein T22E16.160
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 26-May-2000
C:Accession: T47689
R:Benes, V.; Wurmback, E.; Drzonek, H.; Ansoerge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.
submitted to the Protein Sequence Database, February 2000
A:Reference number: Z24472
A:Accession: T47689
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-260 <BEN>
A:Cross-references: EMBL:AL132975
A:Experimental source: cultivar Columbia; BAC clone T22E16
C:Genetics:
A:Map position: 3
A:Introns: 52/1; 158/2
A:Note: T22E16.160
C:Superfamily: expansin

Query Match	70.2%;	Score 979;	DB 2;	Length 260;
Best Local Similarity	67.5%;	Pred. No. 1.5e-75;		
Matches 172;	Conservative 28;	Mismatches 45;	Indels 10;	Gaps 21

```

QY 6 SPFSSLFLLPFFPVFTFADY-----GWMQSGHAIFYGGDASGTMGACGYNLYSQ 57
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 NPLILLTIFPLFLLLSFTDAGIPRVFSGSGSMQTAAHTFYGGNDASGTMGACGYNLYSQ 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 58 GYGTNTVALSTALFNNGLSGCACEMTCTNDPKWCLPG--TIRVTATNFCPPNFALPNN 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 GYGTNTAALSTLFSNGQSCGACEIKCVNDPKWCHPNPSVFVTATNFCPPNLAQPSDN 123
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 116 GWCNCPLOHFDMAEPAPLQIAOYRAGIVPVSFRVPCMKKGVRFTINGHSYFNLVLT 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 124 GWCNCPRSHFDLAMPVFLKIAEYRAGIVPISYRVRACRKSIGIRFTINGHRYFNLVLT 183
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 176 NVGAGADVHSVSIKGSRTGWMQSMRNNQNMQSNNYLNGQGLSFQVTLTSDRTLAYNLV 235
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 184 NVAGAGDIARTSVKGSXTGWMSLTRNNQNMQSNNAVLVGQSLSFRTVSSDRRTSTSWNIA 243
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 236 PSNMQFGQTYEGPOF 250
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 244 PSNMQFGQTYEGKNP 258
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 15

expansin 1 - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 26-May-2000
C:Accession: T07630
R:Rose, J.K.C.; Lee, H.H.; Bennett, A.B.
Proc. Natl. Acad. Sci. U.S.A. 94, 5955-5960, 1997
A:Title: Expression of a divergent expansin gene is fruit-specific and ripening-regulated
A:Reference number: Z16063; MUID:97303239; PMID:9159182
A:Accession: T07630
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-261 <ROS>
A:Cross-references: EMBL:U82123; NID:g2062420; PIDN:AAC63088.1; PID:g2062421
A:Experimental source: cultivar Castlemart; fruit
C:Genetics:
A:Gene: EXP1
A>Note: specifically expressed in ripening fruit, regulated by ethylene
C:Superfamily: expansin

Query Match

68.18; Score 949.5; DB 2; Length 261;

Best Local Similarity 65.8%; Pred. No. 4.8e-73;
Matches 169; Conservative 29; Mismatches 40; Indels 19; Gaps 3;

```
QY 13 LLPFVFTFADY-----GWSGHATFYGGDASGTMGACGYGNLYSQ 57
   :| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3 IIFILVLLFVDSCFNIVEGRIPGVYSGGSMETAHTFYGGSDASGTMGACGYGNLYSQ 62

QY 58 GYGTNTVALSTALFNNGLSGACFEMTCTNDP--KMCLPG--TIRVTATNFCPPNFALPN 113
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 63 GYGVNTAALSTALFNNGLSGACFELKCTNTPNWKWCLPGNPSILITATNFCPPNFALPN 122

QY 114 NNGWCNPPLOHFDMAEPALQIAQYRAGIVPVSFRVPKMKKGVRFTINGHSYENLV 173
   :| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 123 DNGWCNPPRPHFDLAMPMLKLAQYRAGIVPVTYRRIPCRKGGIRFTINGFRYENLV 182

QY 174 ITNVGAGDVHSVSIKSGRTGWSMRNWQNSNNYLNQGLSFQVTLSDGRTLTAYN 233
   ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 183 ITNVAGAGDIKVMWVGITKTNIPLSRNWQNSNAVLTGQSLFRVKASDHRSSISWN 242

QY 234 LVPSNWQFGQTYEGPQF 250
   :| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 243 MYPSTWQFGQTFIGKNF 259
```

Search completed: December 18, 2003, 17:50:20
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 17:45:48 ; Search time 18 Seconds

(without alignments)
653.149 Million cell updates/sec

Title: US-09-383-579C-10

Perfect score: 1394

Sequence: 1 MAFSYPSSSLFLPFFVF.....AYNLVPSNMVQGTVEGPGF 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1085	77.8	253	1 EXP8_ARATH	Q22874 arabidopsis
2	1041	74.7	249	1 EX10_ARATH	Q91dr9 arabidopsis
3	1036.5	74.4	250	1 EXP1_ARATH	Q9c554 arabidopsis
4	1030	73.9	255	1 EXP2_ARATH	Q38866 arabidopsis
5	1024	73.5	248	1 EX15_ARATH	O80622 arabidopsis
6	993	71.2	257	1 EXP4_ARATH	O48818 arabidopsis
7	979	70.2	260	1 EX16_ARATH	Q9m289 arabidopsis
8	965	69.2	255	1 EX14_ARATH	Q9fma0 arabidopsis
9	944	67.7	262	1 EXP3_ARATH	O80932 arabidopsis
10	939	67.4	259	1 EXP6_ARATH	Q38865 arabidopsis
11	934	67.0	258	1 EXP9_ARATH	Q91z99 arabidopsis
12	889.5	63.8	255	1 EXP5_ARATH	Q38864 arabidopsis
13	865.5	62.1	252	1 EX11_ARATH	Q91nu3 arabidopsis
14	838.5	60.2	255	1 EX17_ARATH	Q9zsl1 arabidopsis
15	748	53.7	273	1 EX22_ARATH	Q9f180 arabidopsis
16	741	53.2	279	1 EX26_ARATH	Q9f178 arabidopsis
17	735	52.7	269	1 EX23_ARATH	Q9f179 arabidopsis
18	735	52.7	276	1 EX25_ARATH	Q9f177 arabidopsis
19	718.5	51.5	262	1 EXP7_ARATH	Q91n94 arabidopsis
20	711.5	51.0	312	1 EX24_ARATH	Q9f176 arabidopsis
21	692	49.6	257	1 EX18_ARATH	Q9m9p0 arabidopsis
22	679.5	48.7	266	1 EX13_ARATH	Q9m9p0 arabidopsis
23	669	48.0	252	1 EX12_ARATH	Q91dj3 arabidopsis
24	613	44.0	256	1 EX21_ARATH	Q9f181 arabidopsis
25	604	43.3	256	1 EX20_ARATH	Q9szm1 arabidopsis
26	283.5	20.3	264	1 EXB3_ARATH	Q9m012 arabidopsis
27	279	20.0	271	1 EXB1_ARATH	Q9skuz2 arabidopsis
28	276.5	19.8	273	1 EXB2_ARATH	Q9shy6 arabidopsis
29	273	19.6	259	1 EXB4_ARATH	Q9shd1 arabidopsis
30	245	17.6	269	1 EXBA_MAIZE	P58738 zea mays (m
31	239	17.1	263	1 MPPI_PHLPR	P43213 phleum prat
32	232.5	16.7	265	1 MPH1_HOLLA	P43216 holcus lana
33	229	16.4	263	1 MPL1_LOLPR	P14946 lolium pere

34	228	16.4	246	1 MPCL_CYNDA	O04701 cynodon dac
35	220.5	15.8	269	1 MPAL_PHAHQ	Q41260 phalaris aq
36	217.5	15.6	265	1 EXL1_ARATH	Q91zr4 arabidopsis
37	209	15.0	263	1 EXL3_ARATH	Q91zr5 arabidopsis
38	206.5	14.8	250	1 EXR1_ARATH	O23547 arabidopsis
39	206	14.8	265	1 EXL2_ARATH	Q9sves4 arabidopsis
40	203.5	14.6	264	1 EXB5_ARATH	Q9m203 arabidopsis
41	192.5	13.8	263	1 MPO1_ORYSA	Q40638 oryza sativ
42	185	13.3	191	1 EXB2_MAIZE	Q07154 zea mays (m
43	112.5	8.1	242	1 GUN5_TRIRE	P43317 trichoderma
44	111.5	8.0	123	1 EXR2_ARATH	Q9m0c2 arabidopsis
45	99	7.1	1385	1 YMS5_CAEEL	P34501 caenorhabdi

ALIGNMENTS

RESULT 1
EXP8_ARATH STANDARD; PRT; 253 AA.
ID EXP8_ARATH
AC Q22874;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-expansin 8 precursor (At-EXP8) (AtEx8) (At-ExpAlpha-1.11).
GN EXP8 OR AT2G40610 OR T2P4.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RC MEDLINE=20083487; PubMed=10617197;
RX Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronan L.A., Shen M., Pal G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Niernan W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768(1999).
CC -!- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cell-wall bound.
CC -!- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -!- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -!- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -!- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansins/".

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DR EMBL; AC002336; AAB87577.1; -
DR PIR; F84831; F84831.
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_lool_pi.
DR InterPro; IPR007117; Expan_lool_pi_C.
DR Pfam; PF01357; Pollen allergen; 1.
DR PRINTS; PR01225; EXPANSNFAMILY.
DR ProDom; PD002179; Expan_lool_pi_C; 1.

```

DR PROSITE; PS50843; EXPANSIN CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
KW Cell wall; signal; Multigene family.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 253 ALPHA-EXPANSIN 8.
FT DOMAIN 48 160 EXPANSIN-LIKE EG45.
FT DOMAIN 170 250 EXPANSIN-LIKE CBD.
SQ SEQUENCE 253 AA; 27260 MW; 08C42880D523DD8A CRC64;

Query Match 77.8%; Score 1085; DB 1; Length 253;
Best Local Similarity 77.9%; Pred. No. 1.7e-85;
Matches 194; Conservative 22; Mismatches 31; Indels 2; Gaps 2;

QY 4 SYSPFSSFLLPFFV-FTFADYGMQSGHATFYGGDASGTMGACGYGNLYSGYGTN 62
DB 5 SYLKYSIIISIVLFQGTGDDGCMQGHATFYGGEDASGTMGACGYGNLYGGYGTN 64
QY 63 TVALSTALFNNGLSCGACFEMTCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGMCNPP 122
DB 65 TAAISTALFNNGLTGACYEMKCNDPDRWCLGSTITVTATNFCPPNGLSNDNGMCNPP 124
QY 123 LQHFDMABEPAFLQIAYRAGIVPVSRPVCMKKGVRFTINGHSYFNLVLTNVGAGD 182
DB 125 LQHFDMABEPAFLQIAYRAGIVPVSRPVCMKKGIRFTINGHSYFNLVLTNVGAGD 184
QY 183 VHSVSIKGSRT-GWQMSRNMWQNMWNNYLNQGLSFQVTLSDGRTLTAYNLVPNSWQF 241
DB 185 VHAWSIKGSKTQSWQMSRNMWQNMWNNYLNQGLSFQVTLSDGRTLTAYNLVPNSWQF 244
QY 242 GQTYEGPQF 250
DB 245 GQTYEGGQF 253

```

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RESULT 2
EX10 ARATH STANDARD; PRT; 249 AA.
ID Q9LDR9;
AC Q9LDR9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-expansin 10 precursor (At-EXP10) (AtEX10) (Ath-ExpAlpha-1.1).
GN EXP10 OR AT1G26770 OR T24P13_14 OR T24P13.15.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Alfafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziali A.,
RA Miltischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

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RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vayberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820 (2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT SGP consortium (Salk/Stanford/PEGC).";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found. Plays a
CC major role in control of leaf growth and influences the mechanical
CC breakage behavior of the pedicel.
CC -1- SUBCELLULAR LOCATION: Cell-wall bound.
CC -1- TISSUE SPECIFICITY: Most highly expressed in the young leaf
CC petiole and midrib, in trichomes and at the base of the pedicel.
CC -1- DEVELOPMENTAL STAGE: Expression is first seen at the base of the
CC emerging first two true leaves but not of the cotyledons. As leaf
CC development progresses expression begins in the base of the
CC petiole and gradually extends toward the whole midrib and later it
CC is restricted to the vasculature of the petiole and leaf blade and
CC disappears as the leaf matures.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -1- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -1- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -1- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansins/".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF229437; AAF61712.1; -
DR EMBL; AF229431; AAF61713.1; -
DR EMBL; AC006535; AAF87031.1; -
DR EMBL; AY052247; AAK97717.1; -
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_lo1_pi.
DR InterPro; IPR007117; Expan_lo1_pi_C.
DR Pfam; PF01357; Pollen_allergen.1.
DR PRINTS; PR01225; EXPANSINFAMILY.
DR PRODOM; PD002179; Expan_lo1_pi_C.1.
DR PROSITE; PS50843; EXPANSIN CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
KW Cell wall; signal; Multigene family.
FT SIGNAL 21 POTENTIAL.
FT CHAIN 22 249 ALPHA-EXPANSIN 10.
FT DOMAIN 44 156 EXPANSIN-LIKE EG45.
FT DOMAIN 166 245 EXPANSIN-LIKE CBD.
SQ SEQUENCE 249 AA; 26428 MW; 63D014410D4ABBA1 CRC64;

Query Match 74.7%; Score 1041; DB 1; Length 249;
Best Local Similarity 79.6%; Pred. No. 9.1e-82;
Matches 179; Conservative 23; Mismatches 23; Indels 0; Gaps 0;

QY 26 GGMQSGHATFYGGDASGTMGACGYGNLYSGYGTNTVALSTALFNNGLSCGACFEMTC 85
DB 24 GGMWNAHATFYGGDASGTMGACGYGNLYSGYGTSTALSTALFNNGLSCGSCFIRIC 83
QY 86 TNDPKWCLPGTIRVTATNFCPPNFALPNNNGMCNPPLOHFDMAEPAFLQIAYRAGIVP 145
DB 84 ENDGKWCLPGSIVTATNFCPPNFALPNNNGMCNPPLEHFDLAQPVFORIAYRAGIVP 143
QY 146 VSPRRVPCMKKGVRFTINGHSYFNLVLTNVGAGADVHSVSIKGSRTGWQMSRNMWQF 205

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Db      144 VSYRRVPCRRRGIRFTINGHSYFNLVLITNVGAGDVHSAIKGSRTWQMSRNWGN 203
QY      206 WQSNMYLNGGGLSFQVTLSDGRTLTAYNLVPSPWQFGQTYEGPQF 250
Db      204 WQSNMYLNGGGLSFQVTLSDGRTLTAYNLVPSPWQFGQTYEGPQF 248

RESULT 3
EXPI_ARATH STANDARD; PRT; 250 AA.
AC Q9C554; Q38863;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-expansin 1 precursor (At-EXPI) (AtEx1) (Ath-ExpAlpha-1.2).
GN EXP1 OR AT1G69530 OR F10D13.18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewart K.,
RA Dunn P., Elgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huzar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Miltschker J., Miranda M., Nguyen M., Niernman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT SSP consortium (Salk/Stanford/PGEC).";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 14-250 FROM N.A.
RX MEDLINE=96016146; PubMed=7568110;
RA Shcherban T.Y., Shi J., Durachko D.M., Gultinan M.J.,
RA McQueen-Mason S.J., Shieh M., Cosgrove D.J.;
RT "Molecular cloning and sequence analysis of expansins - a highly
RT conserved, multigene family of proteins that mediate cell wall
RT extension in plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
RN [4]
RP TISSUE SPECIFICITY.
RA Durachko D.M., Cosgrove D.J.;
RT "Expression patterns for selective expansin genes in Arabidopsis.";
RL (In) Abstracts of Plant Biology '99: The annual meeting of the
RL American Society of Plant Physiologists, abstract#56, Baltimore
RL (1999).
CC -i- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found (By
CC similarity).
CC -i- SUBCELLULAR LOCATION: Cell-wall bound.

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CC -i- TISSUE SPECIFICITY: Expressed in stomatal guard cells and very
CC young vascular bundles throughout the plant.
CC -i- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -i- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -i- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -i- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansins/".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AC073178; AAG60095.1; -
DR EMBL; AF360291; AAK26001.1; -
DR EMBL; AY051047; AAK93724.1; -
DR EMBL; AY058193; AAL25606.1; -
DR EMBL; U30476; AAB38070.1; -
DR PIR; T50654; T50654.
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_lo1_pi.
DR InterPro; IPR007117; Expan_lo1_pi_c.
DR Pfam; PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSIN_FAMLY.
DR ProDom; PD002179; Expan_lo1_pi_C; 1.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
DR Cell wall; Signal; Multigene family.
KW SIGNAL
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 250 ALPHA-EXPANSIN 1.
FT DOMAIN 45 157 EXPANSIN-LIKE EG45.
FT DOMAIN 167 246 EXPANSIN-LIKE CBD.
FT CONFLICT 14 18 AMTSH -> NSARD (IN REF. 1).
SQ SEQUENCE 250 AA; 26518 MW; 1D95EBA24FCFE7E5 CRC64;

Query Match 74.4%; Score 1036.5; DB 1; Length 250;
Best Local Similarity 73.6%; Pred. No. 2.2e-81;
Matches 181; Conservative 25; Mismatches 31; Indels 9; Gaps 1;

QY 13 LLPFFVFTFADY-----GGWQGHATFYGGGDASGTMGACGYENLYSQGYGNT 63
Db 3 LVTFLFTLGTAMTSHVNGYAGGWMVNAHATFYGGGDASGTMGACGYENLYSQGYGNT 62

QY 64 VALSTALFNNGLSGACFEEMTCTNDPKKCLPGTIRVTATNFCPPNFALPNNNGWCNPPL 123
Db 63 AALSTALFNNGLSGACFEIRCONDKKCLPGSIVTATNFCPPNNALPNNAGWCNPPL 122

QY 124 QHFDMAEPALQIAQYRAGIVPVSFRYPCKMKKGVRFTINGHSYFNLVLITNVGAGDV 183
Db 123 QHFDLSQVEFQRIAQYRAGIVPVAYRRVPCVRRGIRFTINGHSYFNLVLITNVGAGDV 182

QY 184 HVSISIKGRTGQMSRNMWQSNMYLNGGGLSFQVTLSDGRTLTAYNLVPSPWQFGQ 243
Db 183 HSAMVKGSGRTGQMSRNMWQSNMYLNGGGLSFQVTLSDGRTIVSNVNAVAGWSFGQ 242

QY 244 TYEGPQ 249
Db 243 TFTGAQ 248

RESULT 4
EXPI_ARATH STANDARD; PRT; 255 AA.
AC Q38866; Q9FLC5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-expansin 2 precursor (At-EXPI2) (AtEx2) (Ath-ExpAlpha-1.12).
GN EXP2 OR AT5G05290 OR K18123.9.
OS Arabidopsis thaliana (Mouse-ear cress).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96016146; PubMed=7568110;
RA Shcherban T.Y., Shi J., Durachko D.M., Guiltinan M.J.,
RA McQueen-Mason S.J., Shieh M., Cosgrove D.J.;
RT "Molecular cloning and sequence analysis of expansins - a highly
RT conserved, multigene family of proteins that mediate cell wall
RT extension in plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=98344145; PubMed=9679202;
RA Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
RT features of the regions of 1,381,565 bp covered by twenty one
RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:131-145(1998).
CC -1- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cell-wall bound.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -1- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -1- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -1- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansins/".
CC -----
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CC -----
DR EMBL, U30481; AAB38073.1; -.
DR EMBL, AB010692; BAB09972.1; -.
DR PIR, T50656; T50656.
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_lo1_pi.
DR InterPro; IPR007117; Expan_lo1_pi_C.
DR Pfam; PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSINFAMILY.
DR ProDom; PD002179; Expan_lo1_pi_C; 1.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
KW Cell wall; Signal; Multigene family.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 255 ALPHA-EXPANSIN 2.
FT DOMAIN 50 162 EXPANSIN-LIKE EG45.
FT DOMAIN 172 252 EXPANSIN-LIKE CBD.
FT CONFLICT 88 88 T -> Q (IN REF. 2).
SQ SEQUENCE 255 AA; 27722 MW; 27B5F0827A285500 CRC64;
Query Match 73.9%; Score 1030; DB 1; Length 255;
Best Local Similarity 73.6%; Pred. No. 8.1e-81;
Matches 184; Conservative 29; Mismatches 35; Indels 2; Gaps 2;
OY 3 FSYSPFSSLLFLPF-FEVFTFADYGGWQSGHATFYGGDASGTMGACGYNLVSGYGT 61
Db 6 YSHILFLSLCTLNFCLYSINSDNGWGRGHATFYGGADASGTMGACGYNLVSGYGL 65
OY 62 NTVALSTALFNNGLSCGACFEMTCTNDPKCLPGTIRVATATNFCPPNFALPNNNGWCNP 121
Db 66 QTAALSTALFNSGQKGCACFELTCEDDDEWCIPIGSIIVSATNFCPPNFALANDNGWCNP 125

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OY 122 PLOHFDMAEPAPLQIAQYRAGIVPSFRVPCKMKGVRFTINGHSYENLVLTNVGAG 181
Db 126 PLKHFDLAEPAFLQIAQYRAGIVPAFRVPCERKGGIRFTINGNPYFDLVLTNVGAG 185
OY 182 DVHSVSIKGSRTG-WQSMRRNGQWQSNNTYLNQGLSFQVTLSDGRTLTAYNLVPSNWQ 240
Db 186 DIRAVSLKSKTDQWQSMRRNGQWQSNNTYLRQGLSFQVTLSDGRTLTVSYDVVPHDWQ 245
OY 241 FGQTEGPOF 250
Db 246 FGQTEGGQF 255
RESULT 5
EX15 ARATH STANDARD; PRT; 248 AA.
ID EX15 ARATH STANDARD; PRT; 248 AA.
AC 080622;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-expansin 15 precursor (At-EXP15) (Atex15) (Ath-Expalpha-1.3).
GN EXP15 OR AT2G03090 OR T17M13.26.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pat G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
CC -1- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cell-wall bound.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -1- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -1- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -1- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansins/".
CC -----
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CC -----
DR EMBL, AC004138; AAC32927.1; -.
DR PIR, C84444; C84444.
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_lo1_pi.
DR InterPro; IPR007117; Expan_lo1_pi_C.
DR Pfam; PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSINFAMILY.
DR ProDom; PD002179; Expan_lo1_pi_C; 1.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
KW Cell wall; Signal; Multigene family.
FT SIGNAL 1 20 POTENTIAL.

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FT CHAIN 21 248 ALPHA-EXPANSIN 15.
FT DOMAIN 43 155 EXPANSIN-LIKE EG45.
FT DOMAIN 165 244 EXPANSIN-LIKE CBD.
SQ SEQUENCE 248 AA; 26482 MW; 29E3199269B71271 CRC64;

Query Match 73.5%; Score 1024; DB 1; Length 248;
Best Local Similarity 78.1%; Pred. No. 2.5e-80;
Matches 175; Conservative 23; Mismatches 26; Indels 0; Gaps 0;

QY 27 GWSGHATFYGGSDSGTMGACGYNLYSQGYGTNTVALSTALFNNGLSCGACFEMTCT 86
D 24 GWNVAHATFYGGSDSGTMGACGYNLYSQGYGTNTVALSTALFNNGLSCGACFEMTCT 83
QY 87 NDRKWCLEPGTIRVATNFCPPNFALPNNNGWCNPPLOHFDMAEPFLQIAQYRAGIVPV 146
D 84 SDGAWCLPGAITVATNFCPPNFALPNNNGWCNPPLOHFDLSQPVFQRIAQYRAGIVPV 143
QY 147 SFRVPCMKKGAVFTINGHSYFNLVLTNVGAGDVHSVSIKSGRTGWSMSRNWGQNM 206
D 144 SYRVPFCMRGGIRFTINGHSYFNLVLTNVGAGDVHSVAVKSGRTRWQMSRNWGQNM 203
QY 207 QSNVYNGQGLSFQVTLSDGRTLTAVNLVPSNMQGYEGPOF 250
D 204 QSNVYNGQGLSFQVTLSDGRTLTAVNLVPSNMQGYEGPOF 247

RESULT 6
EXP4_ARATH STANDARD; PRT; 257 AA.
AC 048818;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Alpha-expansin 4 precursor (At-EXP4) (AtEx4) (Ath-ExpAlpha-1.6).
GN EXP4 OR ATG39700 OR F17A14.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.S., Ketchum K.A., Lee J.J., Romling C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Niernman W.C., White O., Eissen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana."
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT SSP consortium (Salk/Stanford/EGEC).";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP TISSUE SPECIFICITY.
RA Durachko D.M., Cosgrove D.J.;
RT "Expression patterns for selective expansin genes in Arabidopsis.";
RL (in) Abstracts of Plant Biology '99: The annual meeting of the
RL American Society of Plant Physiologists, abstract#56, Baltimore
RL (1999).
CC -!- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found (By
CC similarity).

```

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CC -!- SUBCELLULAR LOCATION: Cell-wall bound.
CC -!- TISSUE SPECIFICITY: Expressed in the vascular bundles throughout
CC the plant.
CC -!- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -!- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -!- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -!- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansin/".
CC -----
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CC -----
CC EMBL; AC003674; AAB97125.1; -.
CC EMBL; AF410277; AAK95263.1; -.
CC PIR; D84820; D84820.
CC InterPro; IPR007112; Expan_endogl.
CC InterPro; IPR007118; Expan_lo1_pi.
CC InterPro; IPR007117; Expan_lo1_pi_C.
CC Pfam; PF01357; Pollen_allergen.1.
CC PRINTS; PR01225; EXPANSIN_FAMLY.
CC ProDom; PD002179; Expan_lo1_pi_C.1.
CC PROSITE; PS50843; EXPANSIN_CBD.1.
CC PROSITE; PS50842; EXPANSIN_EG45.1.
CC Cell wall; Signal; Multigene family.
CC SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 257 ALPHA-EXPANSIN 4.
FT DOMAIN 49 163 EXPANSIN-LIKE EG45.
FT DOMAIN 173 252 EXPANSIN-LIKE CBD.
SQ SEQUENCE 257 AA; 27847 MW; 5C510E930A35B736 CRC64;

Query Match 71.2%; Score 993; DB 1; Length 257;
Best Local Similarity 71.4%; Pred. No. 1.2e-77;
Matches 177; Conservative 24; Mismatches 37; Indels 10; Gaps 2;

QY 13 LLPFFVFTFADY-----GWSGHATFYGGSDSGTMGACGYNLYSQGYGTNTV 64
D 8 LFTTFVLFSLDARIPGIYSGAWQNAHATFYGGSDSGTMGACGYNLYSQGYGTNTA 67
QY 65 ALSTALFNNGLSCGACFEMTCTNDPKWCLPG--TIRVTATNFCPPNFALPNNNGWCNPP 122
D 68 ALSTALFNNGLSCGACFELKCANPDQWCHSGSPSILITATNFCPPNFALPNSDNGWCNPP 127
QY 123 LQHFMAEPFLQIAQYRAGIVPVSRVPCMKKGAVFTINGHSYFNLVLTNVGAGD 182
D 128 REHFDLAMPVFLKIAQYRAGIVPVSRVPCMKKGAVFTINGHSYFNLVLTNVAGAGD 187
QY 183 VHSVSIKSGRTGWSMSRNWGQNMNSNNYNGQGLSFQVTLSDGRTLTAVNLVPSNMQFG 242
D 188 IVRASVKGSRGTGWSMSLSRNWGQNMNSNAVLVQALSFRVTGSDRRTSTSMNVPSNMQFG 247
QY 243 QTYEGPOF 250
D 248 QTFVGKNF 255

RESULT 7
EXP4_ARATH STANDARD; PRT; 260 AA.
AC 09M259;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-expansin 16 precursor (At-EXP16) (AtEx16) (Ath-ExpAlpha-1.7).
GN EXP16 OR ATG55500 OR T22E16.160.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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OX NCB1_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unsel'd M., Obermaier B.,
RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Puigdomenech P.,
RA Deiseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choisme N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Dizonex H., Erfle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Scharfe M., Schoen O., Barges M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Maury D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Malti R., Wu D., Peterson J., Van Aken S.,
RA Pat G., Miltscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.,
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
thaliana.";
RL Nature 408:820-822(2000).
CC -1- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cell-wall bound.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -1- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -1- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -1- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansins/".
CC -----
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CC -----
CC EMBL: AL132975; CAB75908.1; -.
CC FIR; T47689; T47689.
CC InterPro; IPR007112; Expan_endogl.
CC InterPro; IPR007118; Expan_lo1_pi.
CC InterPro; IPR007117; Expan_lo1_pi_c.
CC Pfam; PF01357; Pollen_allergen; 1.
CC PRINTS; PR01225; EXPANSINFAMILY.
CC PRODOM; PD002179; Expan_lo1_pi_C; 1.
CC PROSITE; PS50843; EXPANSIN_CBD; 1.
CC PROSITE; PS50842; EXPANSIN_EG45; 1.
CC Cell wall; Signal; Multigene family.
CC SIGNAL 1 23 POTENTIAL.
CC CHAIN 24 260 ALPHA-EXPANSIN 16.
CC DOMAIN 52 166 EXPANSIN-LIKE EG45.
CC DOMAIN 176 255 EXPANSIN-LIKE CBD.
CC SEQUENCE 260 AA; 28162 MW; 1428C01FCD44E994 CRC64;
Query Match 70.2%; Score 979; DB 1; Length 260;
Best Local Similarity 67.5%; Pred. No. 1.8e-76;
Matches 172; Conservative 28; Mismatches 45; Indels 10; Gaps 2;

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QY 6 SPFSSLLPFPFFVFTFADY-----GQWQGHATFYGGDASGTMGACGYNLYSQ 57
Db 4 NPLILITIFPLFLLSFTDAGIPRVSSGSKWQTAHATFYGGDASGTMGACGYNLYSQ 63
QY 58 GYGTNTVALSTALFNNGLSCGACFEMTCTNDPRKCLPG-TIRVTAATNFCPPNALPNN 115
Db 64 GYGTNTALSTLSFNSGQSCGACFEIKCVNDPRKCHPGNPSVPTATNFCPPNALQPSDN 123
QY 116 GGMGNPPLQHPMAEPALQIAYRAGIVPVPFRVPCMKKGIVRTINGHSYFNVLIT 175
Db 124 GGMGNPVRSHFDLAMPVFLKIAEYRAGIVPISYRVACRKSGLRTINGHRYFNVLIT 183
QY 176 NVGAGDVHVSITKSGRTGQMSRNMGQNNYLNQGLSFQVTLSDGRTLAVNLV 235
Db 184 NVAGAGDIARTSVKSGSKTGMSLTRNMQNMGSNAVLVGQSLSFRTSSDRRTSTSWNIA 243
QY 236 PSNWQFGQTYEGPOF 250
Db 244 PSNWQFGQTFVGKPF 258
RESULT 8
EX14_ARATH STANDARD; PRT; 255 AA.
ID EX14_ARATH
AC Q9FMA0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative alpha-expansin 14 precursor (At-EXP14) (AtEX14) (Ath-
DE ExpAlpha-1.5).
GN EXP14 OR AT5G56320 OR MCD7.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCB1_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=98290546; PubMed=9628582;
RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
RA Tabata S.,
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
RT Sequence features of the regions of 1,456,315 bp covered by nineteen
RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:41-54(1998).
CC -1- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cell-wall bound.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -1- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -1- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -1- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansins/".
CC -----
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CC -----
CC EMBL; AB009049; BAB11259.1; -.
CC InterPro; IPR007112; Expan_endogl.
CC InterPro; IPR007118; Expan_lo1_pi.
CC InterPro; IPR007117; Expan_lo1_pi_c.
CC Pfam; PF01357; Pollen_allergen; 1.
CC PRINTS; PR01225; EXPANSINFAMILY.
CC PRODOM; PD002179; Expan_lo1_pi_C; 1.

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DR PROSITE; PS50843; EXPANSIN CBD; 1.
KW Hypothetical protein, Cell wall; Signal; Multigene family.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 255 PUTATIVE ALPHA-EXPANSIN 14.
FT DOMAIN 47 159 EXPANSIN-LIKE EG45.
FT DOMAIN 169 248 EXPANSIN-LIKE CBD.
SQ SEQUENCE 255 AA; 27733 MW; 22A7DD423381CB4E CRC64;

Query Match.
Best Local Similarity 75.4%; Score 965; DB 1; Length 255;
Matches 169; Conservative 18; Mismatches 37; Indels 0; Gaps 0;

QY 27 GWQSGHATFYGGDASGTMGACGYNLVSGYGTNTVALFNNGLSCGCFEMTCT 86
DB 28 GWVNARATFYGGADASGTMGACGYNLVSGYGTNTVALFNNGLSCGACFOIKCV 87
QY 87 NDPKWCLEPRTIRVTATNFCPPNFALPNNNGWCNPLQHFDMAPFLQIAQYRAGIVPV 146
DB 88 DDPKWCIGITVTGTNFCPPNFALPNNNGWCNPLQHFDMAPFLQIAQYRAGIVPV 147
QY 147 SFRRVPCMKKGVRFTINGHSYFNLVLTNVGAGDVHSVSIKGSRTGWSMSRNWGQNV 206
DB 148 QYRRVACRRKGIKIRFTINGHSYFNLVLTNVGAGDVHSVSIKGSRTGWSMSRNWGQNV 207
QY 207 QSNMYLNGQGLSFQVTLSDGRTLTAYNLVPSPNQFGQTYEGPOF 250
DB 208 QSNAKLDGQALSPFKVTTSDGRTVLSNNATPRNWSFGQTYTGKQF 251

RESULT 9
EXP3_ARATH STANDARD; PRT; 262 AA.
AC O80932;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-expansin 3 precursor (At-EXP3) (AtEx3) (Ath-ExpAlpha-1.9).
GN EXP3 OR AT2G37640 OR F13M22.14.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Rongling C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
CC -!- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cell-wall bound.
CC -!- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -!- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -!- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -!- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansins/".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AC004684; AAC23634.1; -.
DR PIR; T02530; T02530.
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_lool_pi.
DR InterPro; IPR007117; Expan_lool_pi_C.
DR Pfam; PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSIN_FAMILY.
DR ProDom; PD002179; Expan_lool_pi_C; 1.
DR PROSITE; PS50843; EXPANSIN CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
KW Cell wall; Signal; Multigene family.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 262 ALPHA-EXPANSIN 3.
FT DOMAIN 54 168 EXPANSIN-LIKE EG45.
FT DOMAIN 178 257 EXPANSIN-LIKE CBD.
SQ SEQUENCE 262 AA; 28266 MW; AFC4D0EC599B4882 CRC64;

Query Match.
Best Local Similarity 71.8%; Score 944; DB 1; Length 262;
Matches 163; Conservative 27; Mismatches 35; Indels 2; Gaps 1;

QY 26 GWQSGHATFYGGDASGTMGACGYNLVSGYGTNTVALFNNGLSCGCFEMTCT 85
DB 34 GPWQNAHATFYGGDASGTMGACGYNLVSGYGTNTVALFNNGLSCGACFEIKC 93
QY 86 TNDPKWCLEP--TIRVTATNFCPPNFALPNNNGWCNPLQHFDMAPFLQIAQYRAGI 143
DB 94 TDDPRWCVPGNPSILVTATNFCPPNFALPNNNGWCNPLQHFDMAPFLQIAQYRAGI 153
QY 144 VPVSFRRVPCMKKGVRFTINGHSYFNLVLTNVGAGDVHSVSIKGSRTGWSMSRNWG 203
DB 154 VPVSFRRVPCMKKGVRFTINGHSYFNLVLTNVGAGDVHSVSIKGSRTGWSMSRNWG 213
QY 204 QNMQSNMYLNGQGLSFQVTLSDGRTLTAYNLVPSPNQFGQTYEGPOF 250
DB 214 QNMQSNMYLNGQGLSFQVTLSDGRTLTAYNLVPSPNQFGQTYEGPOF 260

RESULT 10
EXP6_ARATH STANDARD; PRT; 259 AA.
AC Q38865; O81065;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-expansin 6 precursor (At-EXP6) (AtEx6) (Ath-ExpAlpha-1.8).
GN EXP6 OR AT2G28950 OR T914.3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=96016146; PubMed=7568110;
RA Shcherban T.Y., Shi J., Durachko D.M., Gultinan M.J.,
RA McQueen-Mason S.J., Shieh M., Cosgrove D.J.;
RT "Molecular cloning and sequence analysis of expansins - a highly
RT conserved, multigene family of proteins that mediate cell wall
RT extension in plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,

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DR Pfam; PF01357; Pollen allergen; 1.
DR PRINTS; PR01225; EXPANSIN_FAMLY.
DR ProDom; PD002179; Expan_Lo1_P1_C; 1.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
KW Cell wall; Signal; Multigene family.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 258 ALPHA-EXPANSIN 9.
FT DOMAIN 50 164 EXPANSIN-LIKE EG45.
FT DOMAIN 174 253 EXPANSIN-LIKE CBD.
SQ SEQUENCE 258 AA; 2749 MW; 61AE7AD0C32A1F19 CRC64;

Query Match
Best Local Similarity 67.0%; Score 934; DB 1; Length 258;
Matches 164; Conservative 21; Mismatches 40; Indels 2; Gaps 1;

QY 26 GGMQSGHATFYGGDASGTWGCAGYGNLYSGYGTNTVALSTALFNNGLSCGACFEMTC 85
DB 30 GPWNAHATFYGEADASGTWGCAGYGNLYSGYGTNTALSTALFNNGLSCGSCFELKC 89
QY 86 TNDPKWCLPG--TIRVTATNFCPPNFALPNNNGWCNPPLOHFDMAEPALQIAQYRAGI 143
DB 90 INDPGWCLPGNSILITATNFCPPNFQASDNGWCNPPREHFDLAMPMLSTAKYKAGI 149
QY 144 VPVSFRVRPCMKKGGVRFITNGHSYFNLVLTNVGAGDVHSVSIKSRGTQMSRNMWG 203
DB 150 VPVSYRRIPCRKKGIRFTINGKFFNLVLTNVAGAGDVIKSVKGSNTQMLDLSRNMWG 209
QY 204 QNMQSNLYNGQGLSFQVTLSDGRTLTAYNLVPSNMWFGQTYEGPQF 250
DB 210 QNMQSNALVQGLSFRVKTSDGRSSTSNNTAPSNWQFGQTYSGKNF 256

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RESULT 12
EXPS_ARATH STANDARD; PRT; 255 AA.
AC Q38864;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-expansin 5 precursor (At-EXP5) (AtEX5) (Ath-ExpAlpha-1.4).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96016146; Pubmed=7568110;
RA Shcherban T.Y., Shi J., Durachko D.M., Gultinan M.J.,
RA McQueen-Mason S.J., Shieh M., Cosgrove D.J.;
RT "Molecular cloning and sequence analysis of expansins - a highly
RT conserved, multigene family of proteins that mediate cell wall
RT extension in plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20277480; Pubmed=10819329;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
CC -!- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cell-wall bound.
CC -!- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -!- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -!- SIMILARITY: Contains 1 expansin-like CBD domain.

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CC -!- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansins/".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U30478; AAB38071.1; -.
DR EMBL; AB025615; BAA95756.1; -.
DR PIR; T50655; T50655.
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_Lo1_P1.
DR InterPro; IPR007117; Expan_Lo1_P1_C.
DR Pfam; PF01357; Pollen allergen; 1.
DR PRINTS; PR01225; EXPANSIN_FAMLY.
DR ProDom; PD002179; Expan_Lo1_P1_C; 1.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
KW Cell wall; Signal; Multigene family.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 255 ALPHA-EXPANSIN 5.
FT DOMAIN 56 161 EXPANSIN-LIKE EG45.
FT DOMAIN 171 250 EXPANSIN-LIKE CBD.
SQ SEQUENCE 255 AA; 27611 MW; 7580595A30DC414B CRC64;

Query Match
Best Local Similarity 63.8%; Score 889.5; DB 1; Length 255;
Matches 157; Conservative 26; Mismatches 34; Indels 9; Gaps 2;

QY 26 GGMQSGHATFYGGDASGTWGCAGYGNLYSGYGTNTVALSTALFNNGLSCGACFEMTC 85
DB 36 GPWNAHATFYGGDASGTWGCAGYGNLYSGYGLFTALSTALFDQGLSCGACFELMC 95
QY 86 TNDPKWCLPG--TIRVTATNFCPPNFALPNNNGWCNPPLOHFDMAEPALQIAQYRAGI 144
DB 96 VNDPQWCLGRSIVTATNFCPP-----GGACDPNNHFDLSQPIYERIALYKSGII 147
QY 145 VPVSFRVRPCMKKGGVRFITNGHSYFNLVLTNVGAGDVHSVSIKSRGTQMSRNMWG 204
DB 148 PVMYRRVRCKRSGGIRFTINGHSYFNLVLTNVGAGDVHSVSMKGSRTKQMLSRNMWG 207
QY 205 NMQSNLYNGQGLSFQVTLSDGRTLTAYNLVPSNMWFGQTYEGPQF 250
DB 208 NMQSNLYNGQGLSFVVTTSDRRSVSVFVAPPTWTFGQTYTGQGF 253

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RESULT 13
EX11_ARATH STANDARD; PRT; 252 AA.
AC Q9LNU3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-expansin II precursor (At-EXP11) (AtEX11) (Ath-ExpAlpha-1.14).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; Pubmed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

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RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizlar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzali A.,
RA Miltseher J., Miranda M., Nguyen M., Niemman W.C., Osborne B.I.,
RA Pai G., Peterson S., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana."
RL Nature 408:816-820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT SSP consortium (Salk/Stanford/PGEC).";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP TISSUE SPECIFICITY.
RA Durachko D.M., Cosgrove D.J.;
RT "Expression patterns for selective expansin genes in Arabidopsis."; (In)
RL Abstracts of Plant Biology '99: The annual meeting of the
RL American Society of Plant Physiologists, abstract#56, Baltimore
(1999).
CC -1- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cell-wall bound.
CC -1- TISSUE SPECIFICITY: Expressed in the leaf, but not in the
CC epidermis or in the vascular bundles.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -1- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -1- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -1- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansins/".
CC -----
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CC -----
DR EMBL; AC022472; AAF79895.1; -
DR EMBL; AF332436; AAG48799.1; -
DR PIR; F86335; F86335.
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_lo1_pi.
DR InterPro; IPR007117; Expan_lo1_pi_C.
DR Pfam; PF01357; Pollen_allergen_1.
DR PRINTS; PR01225; EXPANSINFAMILY.
DR PRODOM; PD002179; Expan_lo1_pi_C; 1.
DR PROSITE; PSS0843; EXPANSIN_CBD; 1.
DR PROSITE; PSS0842; EXPANSIN_EG45; 1.
KW Cell wall; Signal; Multigene family.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 252 ALPHA-EXPANSIN 11.
FT DOMAIN 44 159 EXPANSIN-LIKE EG45.
FT DOMAIN 169 248 EXPANSIN-LIKE CBD.
SQ SEQUENCE 252 AA; 26761 MW; 9CE86DA49BEA931B CRC64;
Query Match 62.1%; Score 865.5; DB 1; Length 252;
Best Local Similarity 69.8%; Pred. No. 8.3e-67;
Matches 155; Conservative 23; Mismatches 41; Indels 3; Gaps 2;

Db	25	GLTNGHATFYGGSDASGTMGACCGYGDLYSAGYGTMTALSTALFNDGASCGECYRITCD	84
Qy	87	N--DPKWCPLPG-TIRVTATNFCPPNFALPNNGGWCNBPLOHFDMAEPFLQIAQYRAGI	1433
Db	85	HAADSRWCLKGASVITATNFCPPNFALPNNGGWCNBPLOHFDMAEPWEKIGIYRGGI	1444
Qy	144	VPVSRFRVPCKMKGGVRFITNGHSTFNVLITNVGACADVHSVSIKSGRTGQMSRNVG	2033
Db	145	VPVVFQVRVSCYKKGQVRFIRNGRDFELVNIQNVGAGASIKSVSIKSGRTGWLAMSRNVG	2044
Qy	204	QNMOSNNYLLNGGGLSFQVTLSDGRILTAYNLVPSNMFGQTY	245
Db	205	ANMOSNAYLDGQALSFSITTTDGAIRVFLNVVPSMSFGQIY	246
RESULT 14			
EX17 ARATH			
ID	EX17 ARATH	STANDARD:	PRT: 255 AA.
AC	Q9ZS11;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Putative alpha-expansin 17 precursor (At-EXPI7) (AtEx17) (Ath-expalpa-1.13).		
GN	EXPI7 OR ATAG01630 OR T15B16.16.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosid 11; Brassicales; Brassicaceae; Arabidopsis.		
OX	NCBI_TaxID=3702;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Columbia;		
RX	MEDLINE=20083488; PubMed=10617198;		
RA	Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,		
RA	Pohl T., Dueterhoeft A., Stiekema W., Entian K.-D., Terry N.,		
RA	Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,		
RA	Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,		
RA	Reich M., Delseny M., Puigdomenech P., Watson M., Schmidheini T.,		
RA	Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,		
RA	Vos P., Hohenseil J., Zimmermann W., Wedler H., Ridley P.,		
RA	Langham S.-A., McCullagh B., Bilham L., Robben J.,		
RA	Van der Schuren J., Grymoprez B., Chuang Y.-J., Vandenbussche F.,		
RA	Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,		
RA	Weltzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,		
RA	Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,		
RA	Moeljan P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,		
RA	Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,		
RA	De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,		
RA	Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,		
RA	Clark L., Doggett J., Hall S., Kay M., Lennard N., McIay K., Mayes R.,		
RA	Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,		
RA	Borkova D., Bloeker H., Scharfe M., Grimm M., Loehnert T.-H.,		
RA	Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,		
RA	Gabel C., Fuchs M., Fattmann B., Granderath K., Dauner D., Herzl A.,		
RA	Neumann S., Argirou A., Vitale D., Liguori R., Piravandi E.,		
RA	Massenet O., Quigley F., Clabaud G., Muendlein A., Felber R.,		
RA	Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,		
RA	Chedor F., Cooke R., Berger C., Monfort A., Casacuberta E.,		
RA	Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,		
RA	Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,		
RA	Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,		
RA	Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,		
RA	Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,		
RA	Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,		
RA	Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,		
RA	Stoncking T., Kalicki J., Graves T., Harmon G., Edwards J.,		
RA	Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,		
RA	Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,		
RA	Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,		
RA	Nelson J., Spieth J., Ryan E., Andrews S., Giesel C., Layman D.,		
RA	Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,		
RA	Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,		


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RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.,
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
thaliana."
RL Nature 402:769-777(1999).
CC -1- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cell-wall bound.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -1- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -1- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -1- DATABASE: NAME=EXPANSIN homepage;
CC WWW=http://www.bio.psu.edu/expansins/".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF104919; AAC72858.1; -.
DR EMBL; AL161492; CAB77733.1; -.
DR PIR; T02010; T02010.
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_lo1_pi.
DR InterPro; IPR007117; Expan_lo1_pi_c.
DR Pfam; PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSINFAMILY.
DR PRODOM; PD002179; Expan_lo1_pi_c; 1.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
KW Hypothetical protein; Cell wall; Signal; Multigene family.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 255 PUTATIVE ALPHA-EXPANSIN 17.
FT DOMAIN 46 161 EXPANSIN-LIKE EG45.
FT DOMAIN 171 251 EXPANSIN-LIKE CBD.
SQ SEQUENCE 255 AA; 27715 MW; A33A62D3522A530F CRC64;

Query Match 60.2%; Score 838.5; DB 1; Length 255;
Best Local Similarity 61.8%; Pred. No. 1.7e-64;
Matches 152; Conservative 37; Mismatches 50; Indels 7; Gaps 4;

QY 8 FSSLFLPF--FFVFTFADYGMQSGHATFYGGDASGTWGCAGYGNLYSQGYGTNTV 64
DB 5 FSLVAMIFSTMFEMKISSVSAGWLQAHATFYGSGDASGTWGCAGYGNLYTDGYKTNTA 64

QY 65 ALSTALFNNGLSGACFEMTC--TNDPKWCLPG-TIRVTATNFCPNFALPNNNGWCNP 121
DB 65 ALSTALFNNGKSCGCGCYQLCDATKVPQWCLKGKKSITITATNFCPNFAGASDNGWCNP 124

QY 122 PLQHFDMABEPAFLQIAQYRAGIVPVSFRVPCMKKGVRFTINGHSYFNLVITNVGAG 181
DB 125 PRPHFDMQPAFLTIAKYKAGIVPILYKKGCRSGGMRFITNGRNYPFLVLSNVAGCG 184

QY 182 DVHSVSIKSGRTG-WQMSRNWGMQNMNNYINGQLSFQVTLSDGRTLTAVNLVPSNMQ 240
DB 185 EISKWIKSKSNKMETMSRWGANYQSNYTLNGQSLSFVKQLSDGSIKALNVVPSNMR 244

QY 241 FGQTYE 246
DB 245 FGQSPK 250

```

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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative alpha-expansin 22 precursor (At-EXP22) (AtEx22) (Ath-
DE ExpAlpha-1.15).
GN EXP22 OR AT5G39270 OR K3K3.18 OR K3K3.120.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=98344145; PubMed=9679202;
RA Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
RT features of the regions of 1,381,565 bp covered by twenty one
RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:131-145(1998).
RN [2]
RP CONCEPTUAL TRANSLATION.
RA Cosgrove D.J.;
RL Unpublished observations (DEC-2001).
CC -1- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cell-wall bound.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -1- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -1- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -1- CAUTION: Ref.1 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -1- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansins/".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB010694; BAB09382.1; ALT SEQ.
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_lo1_pi.
DR InterPro; IPR007117; Expan_lo1_pi_c.
DR Pfam; PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSINFAMILY.
DR PRODOM; PD002179; Expan_lo1_pi_c; 1.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
KW Hypothetical protein; Cell wall; Signal; Multigene family.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 273 PUTATIVE ALPHA-EXPANSIN 22.
FT DOMAIN 70 180 EXPANSIN-LIKE EG45.
FT DOMAIN 190 269 EXPANSIN-LIKE CBD.
SQ SEQUENCE 273 AA; 30219 MW; FA43411C2A543136 CRC64;

Query Match 53.7%; Score 748; DB 1; Length 273;
Best Local Similarity 57.8%; Pred. No. 9.2e-57;
Matches 129; Conservative 37; Mismatches 49; Indels 8; Gaps 3;

QY 28 WQSGHATFYG--GGDASGTWGCAGYGNLYSQGYGTNTVALSTALFNNGLSGACFEMT 84
DB 52 WYDARATFYGDHIGD---TQGACGCGNLFQGYGLATAALSTALFNDGYTCGACYEIM 108

QY 85 CTNDPKWCLPGTIRVTATNFCPNFALPNNNGWCNPPLQHFDMABEPAFLQIAQYRAGIV 144
DB 109 CTRDPQWCLPGSVKITATNFCPANYS--KTDTLWCNCPQKXFDLSLAFMLKIAYKAGIV 166

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 17:46:23 ; Search time 35 Seconds
(without alignments)
1843.233 Million cell updates/sec

Title: US-09-383-579C-10
Perfect score: 1394
Sequence: 1 MAFSISPFSSFLFLPFFRVF.....AYNLVPSNMWQFGQTYEGPQF 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1394	100.0	250	10	Q39625 cucumis sat
2	1160.5	83.2	254	10	O82093 prunus arme
3	1152.5	82.7	260	10	O9FNT0 cicer ariet
4	1151.5	82.6	254	10	O9FUM3 prunus aviu
5	1143.5	82.0	245	10	O9LBB2 zinnia eleg
6	1130.5	81.1	253	10	O8LSS7 rumex palus
7	1125	80.7	247	10	O82625 lycopersico
8	1118	80.2	249	10	O9ZP35 nicotiana t
9	1117.5	80.2	253	10	O9SBT1 fragaria an
10	1116.5	80.1	253	10	O9SMD4 rumex palus
11	1116	80.1	254	10	O8RVK6 malus domest
12	1113.5	79.9	253	10	O93XP2 prunus cera
13	1111	79.7	252	10	O9FS30 prunus pers
14	1108	79.5	252	10	O8LSS6 rumex palus
15	1105	79.3	252	10	O8L133 prunus arme
16	1102.5	79.1	255	10	O8RVK4 musa acumin

17	1101.5	79.0	253	10	Q9SMW1 pinus taeda
18	1092	78.3	232	10	P93493 pinus taeda
19	1087	78.0	232	10	P93492 pinus taeda
20	1085	77.8	232	10	P93495 pinus taeda
21	1077	77.3	232	10	P93494 pinus taeda
22	1063	76.3	248	10	O8L5G5 cicer ariet
23	1059	76.0	258	10	O8LKK3 gossypium h
24	1058	75.9	251	10	O946J1 oryza sativ
25	1053	75.5	252	10	O8VWV8 prunus cera
26	1051	75.4	258	10	O49194 gossypium h
27	1050	75.3	249	10	O93XP1 prunus cera
28	1048	75.2	248	10	O8L5G4 cicer ariet
29	1043	74.8	251	10	O40636 oryza sativ
30	1041.5	74.7	247	10	O9M5I7 triphysaria
31	1041	74.7	249	10	O8LET9 arabidopsis
32	1039	74.5	246	10	O946J0 oryza sativ
33	1038	74.5	246	10	P93442 oryza sativ
34	1037	74.4	252	10	O9FUM2 prunus aviu
35	1032	74.0	258	10	O8LKK2 gossypium h
36	1030	73.9	250	10	O8L5S0 rumex palus
37	1030	73.9	250	10	O8L5S1 rumex palus
38	1029	73.8	250	10	O8L5R7 rumex palus
39	1027	73.7	248	10	O8LKJ8 gossypium h
40	1027	73.7	249	10	O9M5I5 triphysaria
41	1027	73.7	253	10	O94KT7 zea mays (m
42	1024	73.5	253	10	O8VYD1 arabidopsis
43	1022	73.3	249	10	O9ZP36 nicotiana t
44	1008.5	72.3	242	10	O9LBB1 zinnia eleg
45	1002	71.9	250	10	O9FVG9 lycopersico

ALIGNMENTS

RESULT 1
ID Q39625 PRELIMINARY; PRT; 250 AA.
AC Q39625;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE Expansin S1.
GN CS-EXPL.
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=3659;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Burpee Pickler;
RX MEDLINE=96016146; PubMed=7568110;
RA Shcherban T.Y., Shi J., Durachko D.M., Gultinan M.J.,
RA McQueen-Mason S.J., Shieh M., Cosgrove D.J.;
RT "Molecular cloning and sequence analysis of expansins--a highly
RT conserved, multigene family of proteins that mediate cell wall
RT extension in plants.";
RT Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
RL -!- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
DR EMBL; U30382; AAB37746.1; .
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_lo1_pi.
DR InterPro; IPR007117; Expan_lo1_pi_C.
DR Pfam; PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSNFAMLY.
DR PRODOM; PD002179; Expan_lo1_pi_C; 1.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
FT CHAIN 24 250 EXPANSIN S1.
SQ SEQUENCE 250 AA; 27215 MW; 60651BC47E4186DA CRC64;
Query Match 100.0%; Score 1394; DB 10; Length 250;
Best Local Similarity 100.0%; Pred. No. 7.1e-118;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFSYSPFSSLLFLPPFFVFTPADYGGWQSGHATFYGGGDASGTMGACGYGNLYSGGYG 60
DB 1 MAFSYSPFSSLLFLPPFFVFTPADYGGWQSGHATFYGGGDASGTMGACGYGNLYSGGYG 60

QY 61 TNTVALSTALFNNGLSCGACFEMTCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGWCN 120
DB 61 TNTVALSTALFNNGLSCGACFEMTCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGWCN 120

QY 121 PPLQHFDMABEPAFLQIAQYRAGIVPVSFRRVPCMKKGVRFTINGHSYFNLVLTNVGGA 180
DB 121 PPLQHFDMABEPAFLQIAQYRAGIVPVSFRRVPCMKKGVRFTINGHSYFNLVLTNVGGA 180

QY 181 GDVHSVSIKGSRTGQMSMRNWQNNQNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMWQ 240
DB 181 GDVHSVSIKGSRTGQMSMRNWQNNQNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMWQ 240

QY 241 FGQTYEGPOF 250
DB 241 FGQTYEGPOF 250

RESULT 2

ID 082093 PRELIMINARY; PRT; 254 AA.

AC 082093;

DT 01-NOV-1998 (TReMBLrel. 08, Created)

DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)

DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)

DE Expansin.

GN PA-Expi.

OS Prunus armeniaca (Apricot).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.

OX NCBI_TaxID=36596;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Bergeon; TISSUE=Nesocarp, and Exocarp;

RA Mbeguie-A-Mbeguie D., Gomez R.-M., Fils-Lycaon B.;

RT "Molecular cloning and nucleotide sequence of expansin 1 (PA-Expi)

RT from apricot fruit.";

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.

DR EMBL; U93167; AAC33529.1; -.

DR InterPro; IPR007112; Expan_endogl.

DR InterPro; IPR007118; Expan_lo1_pi.

DR InterPro; IPR007117; Expan_lo1_pi_C.

DR Pfam; PF01357; Pollen allergen; 1.

DR PRINTS; PR01225; EXPANSNFAMILY.

DR ProDom; PD002179; Expan_lo1_pi_C; 1.

DR PROSITE; PS50843; EXPANSIN_CBD; 1.

DR PROSITE; PS50842; EXPANSIN_EG45; 1.

SQ SEQUENCE 254 AA; 27264 MW; 88068D75932FD0E1 CRC64;

Query Match 83.2%; Score 1160.5; DB 10; Length 254;
Best Local Similarity 82.4%; Pred. No. 8.6e-97;
Matches 206; Conservative 15; Mismatches 28; Indels 1; Gaps 1;

QY 2 AFSYSPFS-SLFLPPFFVFTPADYGGWQSGHATFYGGGDASGTMGACGYGNLYSGGYG 60
DB 5 ALSLAPLALSLVLFNLHLHGAFAADYGGWGAHATFYGGGDASGTMGACGYGNLYSGGYG 64

QY 61 TNTVALSTALFNNGLSCGACFEMTCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGWCN 120
DB 61 TNTVALSTALFNNGLSCGACFEMTCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGWCN 120

QY 121 PPLQHFDMABEPAFLQIAQYRAGIVPVSFRRVPCMKKGVRFTINGHSYFNLVLTNVGGA 180
DB 125 PPLQHFDMABEPAFLQIAQYRAGIVPVSFRRVPCMKKGVRFTINGHSYFNLVLTNVGGA 184

QY 181 GDVHSVSIKGSRTGQMSMRNWQNNQNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMWQ 240

DB 185 GDVHSVSIKGSRTGQMSMRNWQNNQNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMWQ 244

QY 241 FGQTYEGPOF 250
DB 245 FGQTYEGPOF 254

RESULT 3

ID 09FNT0 PRELIMINARY; PRT; 260 AA.

AC 09FNT0;

DT 01-MAR-2001 (TReMBLrel. 16, Created)

DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)

DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)

DE Expansin.

OS Cicer arietinum (Chickpea) (Garbanzo).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids I; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.

OX NCBI_TaxID=3827;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Castellana; TISSUE=Etiolated epicotyl;

RA Dopico B., Sanchez M.A., Labrador B.;

RT "An second expansin is expressed in chickpea epicotyls.";

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.

DR EMBL; AJ291817; CAC19184.1; -.

DR InterPro; IPR007112; Expan_endogl.

DR InterPro; IPR007118; Expan_lo1_pi.

DR InterPro; IPR007117; Expan_lo1_pi_C.

DR InterPro; IPR000504; RNA_rec_mot.

DR Pfam; PF01357; Pollen allergen; 1.

DR PRINTS; PR01225; EXPANSNFAMILY.

DR ProDom; PD002179; Expan_lo1_pi_C; 1.

DR PROSITE; PS50843; EXPANSIN_CBD; 1.

DR PROSITE; PS50842; EXPANSIN_EG45; 1.

DR PROSITE; PS00030; RRM_RNP_1; 1.

SQ SEQUENCE 260 AA; 28266 MW; 32A70368ED2883E9 CRC64;

Query Match 82.7%; Score 1152.5; DB 10; Length 260;
Best Local Similarity 81.9%; Pred. No. 4.7e-96;
Matches 203; Conservative 18; Mismatches 20; Indels 7; Gaps 1;

QY 10 SLFLPPFFVF-----TFADYGGWQSGHATFYGGGDASGTMGACGYGNLYSGGYGTN 62
DB 13 SIVLKGILFLFNNMWSAIDYGGWGAHATFYGGGDASGTMGACGYGNLYSGGYGTN 72

QY 63 TVALSTALFNNGLSCGACFEMTCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGWCNP 122
DB 73 TAAISTALFNNGLSCGSCYEMRCNDPFRWCKPGSIITVATNFCPPNPLANNNGWCNP 132

QY 123 LQHFDMABEPAFLQIAQYRAGIVPVSFRRVPCMKKGVRFTINGHSYFNLVLTNVGAGD 182
DB 133 LQHFDMABEPAFLQIAQYRAGIVPVSFRRVPCMKKGVRFTINGHSYFNLVLTNVGAGD 192

QY 183 VHSVSIKGSRTGQMSMRNWQNNQNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMWQF 242
DB 193 VHSVSIKGSRTGQMSMRNWQNNQNNYLNQGLSFQVTLSDGRTMTSYNVAPSNMWQF 252

QY 243 QTYEGPOF 250
DB 253 QTYEGPOF 260

RESULT 4

ID 09FUM3 PRELIMINARY; PRT; 254 AA.

AC 09FUM3;

DT 01-MAR-2001 (TReMBLrel. 16, Created)

DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)

DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)

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DE Expansin 1.
GN EXP1 OR EXP2.
OS Prunus avium (Cherry), and
OS Prunus cerasus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=42229, 140311;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=P.avium;
RA Wu Z., Wiersma P.A.;
RT "Differential Expression of Expansin Genes Isolated from Sweet Cherry
  (Prunus avium L.) During Fruit Ripening."
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=P.cerasus; TISSUE=Fruit;
RA Yoo S.-D., Gao Z., Cantini C., Loescher W., van Nocker S.;
RT "Coordinated expression of genes encoding expansins and other cell
  wall-modifying enzymes is associated with pectin-related changes in
  the cell wall during ripening of cherry (P. cerasus) fruit."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
DR EMBL; AF297521; AAC13982.1; -
DR EMBL; AF350937; AAK48846.1; -
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_lo1_pi.
DR InterPro; IPR007117; Expan_lo1_pi_C.
DR Pfam; PF01357; Pollen allergen; 1.
DR PRINTS; PRO1225; EXPANSNFAMILY.
DR ProDom; PD002179; Expan_lo1_pi_C; 1.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
SQ SEQUENCE 254 AA; 27278 MW; 953A7EB2491FD0E1 CRC64;

Query Match 82.6%; Score 1151.5; DB 10; Length 254;
Best Local Similarity 82.0%; Pred. No. 5.6e-96;
Matches 205; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 2 AFSYSPFS-SLFLLPFFVFTPADYGGWQSGHATFYGGDASGTMGACGYGNLYSQGYG 60
DB 5 ALSLAPLALSLVLFNLHLHGAFAADYGGWEGAHATFYGGDASGTMGACGYGNLYSQGYG 64

QY 61 TNTVALSTALFNNGLSGCACFEMTCTNDPKWCLPGTIRVATNFPCPNFALPNNNGWCN 120
DB 65 TNTAALSTALFNNGLSGSCGYEMRCNDPRWCPSITVATNFCPPNFAQSDNDNGWCN 124

QY 121 PPLQHPDMAEPALQIAQYRAGIVPVSFRRVPCMKKGVRFTINGHSYFNLVLTNVGA 180
DB 125 PPLQHFDLAEPALQIAQYRAGIVPVTFRRVPCMKKGIRFTINGHSYFNLVLTNVGA 184

QY 181 GDVHSVSIKSGRTGQMSRNMWQNMNSNYLNGQLSFQVTLSDGRTLTAYNLVPSNMQ 240
DB 185 GDVHSVSIKSGRTGQMPSRNMWQNMNSNYLNGQLSFQVTLSDGRTVTNVAFGNMQ 244

QY 241 FGQTYEGPOF 250
DB 245 FGQTFSGGQF 254

RESULT 5
Q9LNB2 PRELIMINARY; PRT; 245 AA.
AC Q9LNB2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Expansin 2.
OS Zinnia elegans.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Campanulids; Asterales; Asteraceae; Asteroideae;
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OC Heliantheae; Zinnia.
OX NCBI_TaxID=34245;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20317189; PubMed=10859177;
RA Im K.H., Cosgrove D.J., Jones A.M.;
RT "Subcellular localization of expansin mRNA in xylem cells."
RL Plant Physiol. 123:463-470(2000).
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
DR EMBL; AF230332; AAF35901.1; -
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_lo1_pi.
DR InterPro; IPR007117; Expan_lo1_pi_C.
DR Pfam; PF01357; Pollen allergen; 1.
DR PRINTS; PRO1225; EXPANSNFAMILY.
DR ProDom; PD002179; Expan_lo1_pi_C; 1.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
SQ SEQUENCE 245 AA; 26201 MW; F66E26114C27B360 CRC64;

Query Match 82.0%; Score 1143.5; DB 10; Length 245;
Best Local Similarity 81.2%; Pred. No. 2.8e-95;
Matches 203; Conservative 20; Mismatches 22; Indels 5; Gaps 1;

QY 1 MAFSYSPFSSFLPFFVFTPADYGGWQSGHATFYGGDASGTMGACGYGNLYSQGYG 60
DB 1 MALSTFTIVSLVSSFNV-----YGGWENGHATFYGGDASGTMGACGYGNLYSQGYG 55

QY 61 TNTVALSTALFNNGLSGCACFEMTCTNDPKWCLPGTIRVATNFPCPNFALPNNNGWCN 120
DB 56 TNTAALSTALFNNGLSGSCGYEMRCNDPRWCLPGSIVVATNFCPPNPGISNDNGWCN 115

QY 121 PPLQHPDMAEPALQIAQYRAGIVPVSFRRVPCMKKGVRFTINGHSYFNLVLTNVGA 180
DB 116 PPLQHFDLAEPALQIAQYRAGIVPISFQVPCVKKGVRFTINGHSYFNLVLTNVGA 175

QY 181 GDVHSVSIKSGRTGQMSRNMWQNMNSNYLNGQLSFQVTLSDGRTLTAYNLVPSNMQ 240
DB 176 GDVHSVSIKSGRTGQMSRNMWQNMNSNYLNGQLSFQVTLSDGRTITSYNVAPSNMQ 235

QY 241 FGQTYEGPOF 250
DB 236 FGQTFQGGQF 245

RESULT 6
Q8L5S7 PRELIMINARY; PRT; 253 AA.
AC Q8L5S7;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Expansin 7 precursor.
GN EXP7.
OS Rumex palustris.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Polygonaceae; Rumex.
OX NCBI_TaxID=50298;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root/shoot junction;
RA Colmer T., Wagemaker C.A.M., Vriezen W., Voeseek L.A.C.J.,
RA Peeters A.J.M.;
RT "The expression of expansin genes in roots during waterlogging of
  Rumex palustris."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
DR EMBL; AF428174; AAM22621.1; -
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_lo1_pi.
DR InterPro; IPR007117; Expan_lo1_pi_C.
DR Pfam; PF01357; Pollen allergen; 1.
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DR PRINTS; PR01225; EXPANSINFAMILY.
 DR Prodom; PD002179; Expan_lo1_pi_C; 1.
 DR PROSITE; PS50843; EXPANSIN_CBD; 1.
 DR PROSITE; PS50842; EXPANSIN_EG45; 1.
 KW Signal.
 FT SIGNAL 1 25 POTENTIAL.
 SQ SEQUENCE 253 AA; 26765 MW; 5AD64CA8563306C7 CRC64;
 Query Match 81.1%; Score 1130.5; DB 10; Length 253;
 Best Local Similarity 81.0%; Pred. No. 4.4e-94;
 Matches 205; Conservative 14; Mismatches 31; Indels 3; Gaps 2;
 QY 1 MAFSISPSSFLLPF--FFVFTFADYGG-WQSGHATFYGGDASGTMGACGYGNLYSQ 57
 DB 1 MAFQAFCLASSLLIAFQHFVSSAFGDYGDWNGGHATFYGGDASGTMGACGYGNLYSQ 60
 QY 58 GYGTNTVALSTALFNNGLSGACFEMTCTNDPKWCLPGTIRVTATNFCPPNFALPNNNG 117
 DB 61 GYGTSTALSTALFNNGLSGACFEMKCTADPRWCIGCVITVTATNFCPPNFALANDNG 120
 QY 118 WCNPLQHFDMAPFLQIAQYRAGIYVPSFRRVPCMKKGVRFTINGHSYFNLVLTNV 177
 DB 121 WCNPLQHFDLAEPFLQIAQYHAGIYVPSFRRVPCGRKGIRFTVNGHSYFNLVLTNV 180
 QY 178 GGADVHSVSIKSGRTGMSRNGQMSNNYLNQGLSFQVTLSDGRTLTAVNLVPS 237
 DB 181 GGADVHSVSIKSGSGGQMSRNGQMSNNYLNQGLSFQVTLSDGRTLTAVNLVPS 240
 QY 238 NMQFGQTEGPOF 250
 DB 241 NMQFGQTEGSOQ 253

RESULT 7
 ID 082625 PRELIMINARY; PRT; 247 AA.
 AC 082625;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE EXPANSIN.
 GN LEXP2.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
 OC NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hypocotyl;
 RA Catala C., Rose J.K.C., Bennett A.B.;
 RT "Hormonal regulation and expression patterns of LEXP2, a new tomato
 RT expansin.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. VFN8;
 RA Caderas D., Muster M., Vogler H., Mandel T., Rose J.,
 RA McQueen-Mason S., Kuhlmeier C.;
 RT "Limited correlation between expansin gene expression and elongation
 RT growth rate.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
 DR EMBL; AF096776; AAC64201.1; -.
 DR EMBL; AJ239068; CAB43197.1; -.
 DR InterPro; IPR007112; Expan_endogl.
 DR InterPro; IPR007118; Expan_lo1_pi.
 DR InterPro; IPR007117; Expan_lo1_pi_C.
 DR Pfam; PF01357; Pollen_allergen; 1.
 DR PRINTS; PR01225; EXPANSINFAMILY.
 DR Prodom; PD002179; Expan_lo1_pi_C; 1.
 DR PROSITE; PS50843; EXPANSIN_CBD; 1.
 DR PROSITE; PS50842; EXPANSIN_EG45; 1.

SQ SEQUENCE 247 AA; 26470 MW; 99E6F53F84F7A3E1 CRC64;
 Query Match 80.7%; Score 1125; DB 10; Length 247;
 Best Local Similarity 81.6%; Pred. No. 1.3e-93;
 Matches 195; Conservative 21; Mismatches 23; Indels 0; Gaps 0;
 QY 12 FLIPFFVFTFADYGGWQSGHATFYGGDASGTMGACGYGNLYSQGYGTNTVALSTALF 71
 DB 9 FLISFCFYSTFADYGGWQTAHATFYGGDASGTMGACGYGNLYSQGYGTNTVALSTALF 68
 QY 72 NNGISGACFEMTCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGWCNPLQHFDMAP 131
 DB 69 NNGITCGACYELTCNNAQWCLOGTITVTATNFCPPNPSLPNNNGWCNPLQHFDMAP 128
 QY 132 AFLQIAQYRAGIYVPSFRRVPCMKKGVRFTINGHSYFNLVLTNVGAGDVHSVSIKS 191
 DB 129 AFLQIAKYKAGIYVPSFRRVPCMKKGIRFTVNGHSYFNLVLTNVGAGDIQSVSIKS 188
 QY 192 RTGQMSRNGQMSNNYLNQGLSFQVTLSDGRTLTAVNLVPSNMQFGQTEGPOF 250
 DB 189 NTGQQMSRNGQMSNNYLNQGLSFQVTLSDGRTLTAVNLVPSNMQFGQTEGPOF 247

RESULT 8
 ID 092P35 PRELIMINARY; PRT; 249 AA.
 AC 092P35;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Alpha-expansin precursor (Fragment).
 GN NT-BXP5.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
 OC NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. BY2;
 RX MEDLINE=99026292; PubMed=9808735;
 RA Link B.M., Cosgrove D.J.;
 RT "Acid-growth response and alpha-expansins in suspension cultures of
 RT bright yellow 2 tobacco.";
 RL Plant Physiol. 118:907-916 (1998).
 CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
 DR EMBL; AF049354; AAC96081.1; -.
 DR InterPro; IPR007112; Expan_endogl.
 DR InterPro; IPR007118; Expan_lo1_pi.
 DR InterPro; IPR007117; Expan_lo1_pi_C.
 DR Pfam; PF01357; Pollen_allergen; 1.
 DR PRINTS; PR01225; EXPANSINFAMILY.
 DR Prodom; PD002179; Expan_lo1_pi_C; 1.
 DR PROSITE; PS50843; EXPANSIN_CBD; 1.
 DR PROSITE; PS50842; EXPANSIN_EG45; 1.
 KW Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 22 POTENTIAL.
 FT CHAIN 23 249 ALPHA-EXPANSIN.
 SQ SEQUENCE 249 AA; 26663 MW; 9B223A43CA952879 CRC64;
 Query Match 80.2%; Score 1118; DB 10; Length 249;
 Best Local Similarity 81.4%; Pred. No. 5.8e-93;
 Matches 201; Conservative 19; Mismatches 23; Indels 4; Gaps 1;
 QY 8 FSSLFLLPFFVF---TFADYGGWQSGHATFYGGDASGTMGACGYGNLYSQGYGTNT 63
 DB 3 FSISLFLFFFSFCHATFADYGGWQNAHATFYGGDASGTMGACGYGNLYSQGYGTNT 62
 QY 64 VALSTALFNNGLSGACFEMTCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGWCNPL 123
 DB 63 AALSTALFNNGLSGACYELTCNNDGQSLQGSIIVTATNFCPPNPSLPNNNGWCNPL 122

QY 124 QHEDMAEPALQIAQYRAGIVPSFRRVPCMKKGVRFTINGHSYFNLVLTNVGAGADV 183
 DB 123 QHFDLAQPAFLQIAKYRAGIVPSFRRVPCRRKGVRFTINGHSFNLVLTNVGAGADV 182
 QY 184 HVSIVKSGRTGQMSRNMWQWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPNNWQFQ 243
 DB 183 QSVSIKGSNTGQWTSRNMWQWQNNANLNGQSLSFQVTLSDGRTLTSNNAPANNWQFQ 242
 QY 244 TYEGPOF 250
 DB 243 TFEGAQF 249

RESULT 9

Q9SBT1 PRELIMINARY; PRT; 253 AA.
 AC Q9SBT1;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Expansin.
 GN EXP2.
 OS Fragaria ananassa (Strawberry).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
 OX NCBI_TaxID=3747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Chandler;
 RA Civello P.M., Sabehat A., Powell A.L.T., Bennett A.B.;
 RT "An expansin gene expressed in ripening strawberry fruit is auxin-
 RT independent.";
 RL Plant Physiol. 12:1273-1279(1999).
 CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
 DR EMBL; AF159563; AAF21101.1;
 DR InterPro; IPR007112; Expan_endogl.
 DR InterPro; IPR007118; Expan_lo1_pi.
 DR InterPro; IPR007117; Expan_lo1_pi.
 DR InterPro; IPR00408; Reg_chr_condens.
 DR Pfam; PF01357; Pollen_allergen; 1.
 DR PRINTS; PR01225; EXPANSINFAMILY.
 DR ProDom; PD002179; Expan_lo1_pi_C; 1.
 DR PROSITE; PS50843; EXPANSIN_CBD; 1.
 DR PROSITE; PS50842; EXPANSIN_EG45; 1.
 DR PROSITE; PS00626; RCC1_2; 1.
 SQ SEQUENCE 253 AA; 26887 MW; CE39CF00ADEAICEF CRC64;

Query Match 80.2%; Score 1117.5; DB 10; Length 253;
 Best Local Similarity 85.3%; Pred. No. 6.5e-93;
 Matches 197; Conservative 15; Mismatches 18; Indels 1; Gaps 1;

QY 21 TFPADYG-GWQSGHATFYGGDASGTMGACGYNLYSQYGTNTVALSTALFNNGLSGGA 79
 DB 23 TYADYGAGWVGHAIFYGGDASGTMGACGYNLYSQYGTNTALSTALFNDGLSCGS 82
 QY 80 CFEMTCTNDPKCLPGTIRVTATNFCPPNFALPNNNGWCNPPLQHFDMAPALQIAQY 139
 DB 83 CYEMRCNDNPRWCLPGSIIVTATNFCPPNFQAQANDNGWCNPPLQHFDAEPALQIAQY 142
 QY 140 RAGIVPSFRRVPCMKKGVRFTINGHSYFNLVLTNVGAGADVHSVSIKSGRTGQMS 199
 DB 143 RAGIVPSFRRVACVKKGGIRFTINGHSYFNLVLTNVAGAGDVHSVSIKSGKQWQMS 202
 QY 200 RNMWQWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPNNWQFQTYEGPOF 250
 DB 203 RNMWQWQSNNYLNGQGLSFQVTLSDGRTVTSNNVAPGNNWQFQTFSGQF 253

RESULT 10
 Q9SWD4 PRELIMINARY; PRT; 253 AA.
 ID Q9SWD4
 AC Q9SWD4;

DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Expansin.
 GN EXP1.
 OS Rumex palustris.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Polygonaceae; Rumex.
 OX NCBI_TaxID=50298;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=leaf;
 RC MEDLINE=20330988; PubMed=10872228;
 RA Vriezen W.H., De Graaf B., Mariani C., Voeselek L.A.C.J.;
 RT "Submergence induces expansin gene expression in flooding-tolerant
 RT Rumex palustris and not in flooding-intolerant R. acetosa.";
 RL Planta 210:956-963(2000).
 CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
 DR EMBL; AF167360; AAD49956.1;
 DR InterPro; IPR007112; Expan_endogl.
 DR InterPro; IPR007118; Expan_lo1_pi.
 DR InterPro; IPR007117; Expan_lo1_pi.
 DR Pfam; PF01357; Pollen_allergen; 1.
 DR PRINTS; PR01225; EXPANSINFAMILY.
 DR ProDom; PD002179; Expan_lo1_pi_C; 1.
 DR PROSITE; PS50843; EXPANSIN_CBD; 1.
 DR PROSITE; PS50842; EXPANSIN_EG45; 1.
 SQ SEQUENCE 253 AA; 27063 MW; 7DC75610C80B23A8 CRC64;

Query Match 80.1%; Score 1116.5; DB 10; Length 253;
 Best Local Similarity 79.4%; Pred. No. 8e-93;
 Matches 201; Conservative 16; Mismatches 33; Indels 3; Gaps 2;

QY 1 MAFSYPSSFLPLPF--FFVFTPADYG-GWQSGHATFYGGDASGTMGACGYNLYSQ 57
 DB 1 MAFQAFLLASSLLLVFQHFISAFGDYGDWNGGHATFYGGDASGTMGACGYGLYSQ 60
 QY 58 GYGTNTVALSTALFNNGISGACFEMTCTNDPKCLPGTIRVTATNFCPPNFALPNNNG 117
 DB 61 GYGTSTALSTALFNNGISGACFEINCTRDPRWCIGVITVTATNFCPPSFALANNNG 120
 QY 118 WCNPLQHFDMAPALQIAQYRAGIVPSFRRVPCMKKGVRFTINGHSYFNLVLTNV 177
 DB 121 WCNPLQHFDAEPALQIAQYHAGIVPSFRRVPCRRKGIRFTVNGHSYFNLVLTNV 180
 QY 178 GGAGDVHSVSIKSGRTGQMSRNMWQWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVP 237
 DB 181 GGAGDVHSVSIKSGRGMQMSRNMWQWQSNYSYLGQSLSFMTTSDGRTLTSFNVAPF 240
 QY 238 NMWQFQTYEGPOF 250
 DB 241 KMWQFQTFEGSQF 253

RESULT 11

Q8RVK6 PRELIMINARY; PRT; 254 AA.
 ID Q8RVK6
 AC Q8RVK6;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Expansin 1.
 GN EXP1.
 OS Malus domestica (Apple) (Malus sylvestris).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.
 OX NCBI_TaxID=3750;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Granny Smith; TISSUE=Ripening fruit pulp;
 RA Trivedi P.K., Solomos T.;

RT	"Characterization of expansin cDNA from apple.";				
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.				
CC	-1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.				
DR	EMBL; AY083166; AAM08928.1; -.				
DR	InterPro; IPR007112; Expan_endogl.				
DR	InterPro; IPR007117; Expan_lo1_pi_C.				
DR	InterPro; IPR000408; Reg_chr_condens.				
DR	Pfam; PF01357; Pollen_allergen; 1.				
DR	ProDom; PD002179; Expan_lo1_pi_C; 1.				
DR	PROSITE; PS50843; EXPANSIN_CBD; 1.				
DR	PROSITE; PS50842; EXPANSIN_EG45; 1.				
DR	PROSITE; PS00626; RCC1_2; 1.				
SR	SEQUENCE 254 AA; 27246 MW; 23FBED3E8B0B3D6D CRC64;				
QY	Query Match	80.1%;	Score 1116;	DB 10;	Length 254;
Db	Best Local Similarity	82.2%;	Pred. No. 9e-93;		
	Matches 198;	Conservative 13;	Mismatches 30;	Indels 0;	Gaps 0
QY	10 SLELLPFFVFPTADYGGWQSGHATFYGGGDASGTMGACGYNLYSGYGTNTVALSTA	69			
Db	14 SLVLFNLHLHGLVLAAYGSGWEGVHATFYGGGDASATMGACGYNLYSGYGTNTALSTA	73			
QY	70 LENNGLSGACGFEMTCTNDPKWCLPGTIRVTATNFCPPNFPALPNNGWCNPPLQHPDMA	129			
Db	74 LENNGLSGSGCYEMMCNNDPRMCRPGSIIVTATNFCPPNFAESNDNGWCNPPLQHPDLA	133			
QY	130 EPAFLQIAQYRAGIIVPSFRRVPCMKKGVRFTINGHSYFNLVLTITVAGAGDVHSVSIK	189			
Db	134 EPAFLQIAQYRAGIIVPSFRRVPCMKKGIRFTINGHSYFNLVLTITVAGAGDVHSVSIK	193			
QY	190 GSRTGWSMSRNRWGQNSNNYLNCGGISFOVTLSDGRTLTAIYLVPSNWQFGQTYEGPO	249			
Db	194 GSRTGQPMPSRNWGQNSNSYLNQALISFOVTTSDGRTVTSYNVAPGNWQFGQTFSGGO	253			
QY	250 F 250				
Db	254 F 254				
RESULT 12					
ID	Q93XP2	PRELIMINARY;	PRT;	253 AA.	
AC	Q93XP2;				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DE	01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
GN	Expansin.				
OS	Prunus cerasus.				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	eurosid1; Rosales; Rosaceae; Amygdaloideae; Prunus.				
OX	NCBI_TaxID=140311;				
RP	[1]				
RC	SEQUENCE FROM N.A.				
RA	TISSUE=fruit;				
RT	Yoo S.-D., Gao Z., Cantini C., Loescher W., van Nocker S.;				
RT	"Coordinated expression of genes encoding expansins and other cell				
RT	wall-modifying enzymes is associated with pectin-related changes in				
RT	the cell wall during ripening of cherry (P. cerasus) fruit.";				
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.				
CC	-1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.				
DR	EMBL; AF350936; AAK48845.1; -.				
DR	InterPro; IPR007112; Expan_endogl.				
DR	InterPro; IPR007118; Expan_lo1_pi				
DR	InterPro; IPR007117; Expan_lo1_pi_C.				
DR	Pfam; PF01357; Pollen_allergen; 1.				
DR	PRINTS; PRO1225; EXPANSINFAMILY.				
DR	ProDom; PD002179; Expan_lo1_pi_C; 1.				
DR	PROSITE; PS50843; EXPANSIN_CBD; 1.				
DR	PROSITE; PS50842; EXPANSIN_EG45; 1.				
SR	SEQUENCE 253 AA; 26861 MW; 9C24484F14AA52CD CRC64;				

[illegible]


```
DB 181 GGAGDVHSVSIKSGRTGMSRNMGNQNSYLNQALSFQVTTSDGRTVTS-NAVPA 239
QY 238 NWQFGQTYEGPOF 250
DB 240 NWQFGQTYEGPOF 252

RESULT 14
Q8L5S6 PRELIMINARY; PRT; 252 AA.
ID Q8L5S6
AC Q8L5S6;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Expansin 8 precursor.
GN EXP8.
OS Rumex palustris.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Polygonaceae; Rumex.
OX NCBI_TaxID=50298;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root/shoot junction;
RA Colmer T., Wagemaker C.A.M., Vriezen W., Voeseek L.A.C.J.,
RA Peeters A.J.M.;
RT "The expression of expansin genes in roots during waterlogging of
RT Rumex palustris."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
DR EMBL; AF428175; AAM22622.1; -
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_lo1_pi.
DR InterPro; IPR007117; Expan_lo1_pi_C.
DR Pfam; PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSNFAMILY.
DR ProDom; PD002179; Expan_lo1_pi_C; 1.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
KW Signal.
FT SIGNAL 1 25 POTENTIAL.
SQ SEQUENCE 252 AA; 26636 MW; 1AFA53C87D81247 CRC64;

Query Match
Best Local Similarity 79.5%; Score 1108; DB 10; Length 252;
Matches 203; Conservative 17; Mismatches 26; Indels 6; Gaps 3;

QY 4 SYSPFSLFLPFFVF---TFADY-GGWSGHATFYGGDASCTMGACGYGNLYSQ 58
DB 2 AFSAFLSASVIFIFGFCIRSGVDYGGWESAHATFYGGDASCTMGACGYGNLYSQ 61

QY 59 YGTNTVALSTALFNNGLSGACFEMTCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGW 118
DB 62 YGTSTAALSTALFNNGLSGACFQMRCSGDPKWLGHITVTATNFCPPNFALPNNNGW 121

QY 119 CNPPLQHFDMAEPAFLQIAQYRAGIVPVSPRRVPCMKKGAVFTINGHSYFNLYLITNVG 178
DB 122 CNPVPQHFDLAEPAFLQIAQYRAGIVPVSP-RVPCGRKGIRFTINGHSYFNLYLITNVG 180

QY 179 GAGDVHSVSIKSGRTGMSRNMGNQNSYLNQGLSFQVTLSDGRTLTAYNLVPSN 238
DB 181 GAGDVHSVSIKSGRTGMSRNMGNQNSYLNQGLSFQVTLSSDGRITVTSNNVAPSG 240

QY 239 WQFGQTYEGPOF 250
DB 241 WQFGQTYEGPOF 252

RESULT 15
ID 081133 PRELIMINARY; PRT; 252 AA.
AC 081133;
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DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Expansin.
GN EXP2.
OS Prunus armeniaca (Apricot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=36596;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bergeon; TISSUE=Mesocarp;
RA Mbeguie-A-Mbeguie D., Fils-Lycaon B.;
RT "Molecular cloning and nucleotide sequence of expansin 2 (Pa-Exp2)
RT from apricot fruit."
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
DR EMBL; AF038815; AAC33530.1; -
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_lo1_pi.
DR InterPro; IPR007117; Expan_lo1_pi_C.
DR Pfam; PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSNFAMILY.
DR ProDom; PD002179; Expan_lo1_pi_C; 1.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
SQ SEQUENCE 252 AA; 26758 MW; 5E81AE5C8E959791 CRC64;

Query Match
Best Local Similarity 79.3%; Score 1105; DB 10; Length 252;
Matches 201; Conservative 23; Mismatches 25; Indels 4; Gaps 4;

QY 1 MAF-SYSPFSLF-LPFFVFVTFADY-GGWSGHATFYGGDASCTMGACGYGNLYSQ 57
DB 1 MAFTHLALIALFVNLCLQGTGYDYGGBEGHATFYGGDASCTMGACGYGNLYSQ 60

QY 58 GYGTNTVALSTALFNNGLSGACFEMTCTNDPKWCLPGTIRVTATNFCPPNFALPNNNG 117
DB 61 GYGTNTALSTALFNNDGLSGSCYEMRCSDPKWCLPGSIITVTATNFCPPNLAQSNNDNG 120

QY 118 WCNPPLQHFDMAEPAFLQIAQYRAGIVPVSPRRVPCMKKGAVFTINGHSYFNLYLITNV 177
DB 121 WCNPPLQHFDLAEPAFLQIAQYRAGIVPVSPRRVSCVKKGIRFTINGHSYFNLYLITNV 180

QY 178 GGAGDVHSVSIKSGRTGMSRNMGNQNSYLNQGLSFQVTLSDGRTLTAYNLVPS 237
DB 181 GGAGDVHSVSIKSGRTGMSRNMGNQNSYLNQGLSFQVTLSSDGRITVTS-NAVPA 239

QY 238 NWQFGQTYEGPOF 250
DB 240 DWQFGQTYEGPOF 252
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Search completed: December 18, 2003, 17:49:48
Job time : 38 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2003, 23:23:52 ; Search time 2047 Seconds
(without alignments)
2968.304 Million cell updates/sec

Title: US-09-383-579C-10
Perfect score: 1394
Sequence: 1 MAFSYPSSSLFLPFFVY.....AYNLVPSNWQFGQTYEGPQF 250

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 segs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09383579/runat_18122003_171927_28784/app_query.fasta_1.391
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09383579 @CGN 1.1 3549 @runat_18122003_171927_28784 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_esthu:*
4: em_estmu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1173.5	84.2	880	14	CD574577	CD574577 UCRPT01_0
2	1153.5	82.7	816	14	CD575807	CD575807 UCRPT01_0
3	1144.5	82.1	809	14	CB291406	CB291406 UCRCS01_0
4	1138	81.6	838	14	CB980842	CB980842 CAB70003
5	1134.5	81.4	799	14	CB293003	CB293003 UCRCS01_0
6	1123.5	80.6	798	10	BG581975	BG581975 EST483712
7	1100.5	78.9	736	14	CD486517	CD486517 CRH3.3F02
8	1099	78.8	772	14	CB980777	CB980777 CAB70003
9	1097.5	78.7	788	14	CB290960	CB290960 UCRCS01_0
10	1081	77.5	767	12	BI932999	BI932999 EST552888
11	1078	77.3	864	14	CB822230	CB822230 EST 3081
12	1070.5	76.8	681	14	CD484188	CD484188 atc01-4mb
13	1061	76.1	815	10	BE131139	BE131139 L48-1090T
14	1060	76.0	747	13	BQ990398	BQ990398 QGF20B04.
15	1059	76.0	685	13	BU815493	BU815493 N042D11.P
16	1056	75.8	816	10	BG645633	BG645633 EST507252
17	1045.5	75.0	770	12	BM780176	BM780176 EST590764
18	1044	74.9	656	13	BQ986992	BQ986992 QGF10P22.
19	1044	74.9	878	14	CD574625	CD574625 UCRPT01_0
20	1043	74.8	786	13	BQ165503	BQ165503 EST611372
21	1042	74.7	868	10	BG446553	BG446553 GA_Eb003
22	1041	74.7	843	14	CB979649	CB979649 CAB70001
23	1039.5	74.6	719	14	CA785153	CA785153 sau25c03
24	1027	73.7	730	14	CA917809	CA917809 EST641956
25	1027	73.7	1106	11	AY104146	AY104146 Zea mays
26	1026	73.6	859	14	CD574696	CD574696 UCRPT01_0
27	1022	73.3	688	14	CB007302	CB007302 VVC043G12
28	1021.5	73.3	723	14	CB292105	CB292105 UCRCS01_0
29	1019	73.1	699	14	CA840495	CA840495 MCT038A10
30	1015	72.8	646	9	AW574064	AW574064 EST316655
31	1014	72.7	656	13	BU892415	BU892415 P063C07.P
32	1013.5	72.7	727	14	CA917661	CA917661 EST641808
33	1008	72.3	966	10	BE055631	BE055631 GA_Ea003
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37	996	71.4	792	12	BI179439	BI179439 EST520384
38	995	71.4	745	9	AW299054	AW299054 EST305728
39	994.5	71.3	733	14	CB978414	CB978414 CAB40005
40	991	71.1	775	10	BE034856	BE034856 ML05C12.M
41	989	70.9	710	12	BI931078	BI931078 EST550967
42	987.5	70.8	754	12	BI978130	BI978130 PH09_O1d
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45	980	70.3	727	14	CA800212	CA800212 sat79e06.

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION UCRPT01_06_G11_T3 Poncirus trifoliata CTV-challenged cDNA library -
ACCESSION CD574577
VERSION CD574577.1 GI:31670479
KEYWORDS EST.
SOURCE Poncirus trifoliata
ORGANISM Poncirus trifoliata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Sapindales; Rutaceae; Poncirus.

REFERENCE 1 (bases 1 to 880)
AUTHORS Roose,M.L., Ye,X., Federici,C.F., Close,T.J., Fenton,R.D.,
TITLE Wanamaker,S., Choi,Y. and Kingan,T.
JOURNAL Development of EST Resources and New Genetic Markers for California
COMMENT Citrus - Poncirus trifoliata CTV-challenged phloem - UCR
Unpublished
Contact: Mikeal Roose
Department of Botany & Plant Sciences, University of California
Riverside, CA, 92521-0124, USA
Tel: 9097874137
Fax: 9097874437
Email: mikeal.roose@ucr.edu
Seq primer: T3.

FEATURES
source location/Qualifiers
1..880
/organism="Poncirus trifoliata"
/mol_type="mRNA"
/cultivar="Pomeroy OP"
/db_xref="taxon:37690"
/clone="UCRPT01_06_G11"
/tissue_type="Phloem"
/dev_stage="10 - 30 cm shoots"
/lab_host="E. coli TJC121"
/clone_lib="Poncirus trifoliata CTV-challenged cDNA library - UCR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; Plants were grown in the greenhouse at University of California, Riverside. The scion was a open-pollinated (very probably selfed) seedling of Poncirus trifoliata cv Pomeroy that was selected as homozygous for the Ctv resistance gene. The rootstock was sweet orange infected with citrus tristeza virus (CTV) isolate T514 over 1 year before sampling. The infects sweet orange, but not genotypes carrying the Ctv resistance gene. Shoots 10-30 cm long were harvested in October 2000, and the green phloem (bark) was removed and frozen quickly in dry ice. Total RNA was extracted using Trizol reagent (Gibco). Poly(A) RNA was purified, a cDNA library was made, and 0.5 million primary lambda cDNA clones were in vivo excised to give a population of pBluescript SK(-) phagemids. All steps to this point were performed in the ML Roose lab at the University of California, Riverside by X. Ye. Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3730 at the University of California Riverside Genomics Institute, Core Instrumentation Facility, (Choi, Kingan). Chromatogram files were transmitted to UC Riverside (by Choi), then processed at UC Riverside (by Wanamaker) using the HarVest pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."

BASE COUNT 231 a 196 c 210 g 243 t
ORIGIN

Alignment Scores:
Pred. No.: 1.14e-99 Length: 880
Score: 1173.50 Matches: 210
Percent Similarity: 90.44% Conservative: 17
Best Local Similarity: 83.67% Mismatches: 23
Query Match: 84.18% Indels: 1
DB: 14 Gaps: 1

US-09-383-579C-10 (1-250) x CD574577 (1-880)

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Db 62 ATTGACATCATCTAGTGTCTCTCTTTGTTGTGCTCAATTTTGTCTTCGTGC 121
QY 21 ThrPheAlaAspTyr---GlyGlyTyrGlnSerGlyHisAlaThrPheTyrGlyGlyGly 39

Db 122 ACATTGGAGACTATGTTGGTGGGTGGCAAAAGTGGCCATGCACCTTTCTATGAGGGCGT 181
QY 40 AspaIaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyr 59
Db 182 GATGCTCCGGCACAATGGGTGGTCTGTGGGTATGGCAATTTGTACAGCCAAAGCTAT 241
QY 60 GlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAla 79
Db 242 GGGACTAACACTGCAGACACTTAGTACCGCTCTATTCAACAATGGCTTAAGCTGTGTTCA 301
QY 80 CysPheGluMetThrCysThrAsnAspProLysTyrCysLeuProGlyThrIleArgVal 99
Db 302 TGGTATGAATGAATGTGAATAATGACCCCAAGTGGTGCTCCCGGCTCCATCATTTGTC 361
QY 100 ThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnGlyGlyTyrCys 119
Db 362 ACCGCCAACCACTTGTGCCACCTTACCTTGCCCTGTCTAACGACAAACGGCGTTGGTGC 421
QY 120 AsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyr 139
Db 422 AATCTCCCTCCACCACTTGTGACATGGCTGAGCCGCTTTCTTGCAAAATGGCCCAATAC 481
QY 140 ArgAlaGlyIleValProValSerPheArgArgValProCysMetLysLysGlyGlyVal 159
Db 482 CGTGCCGATCGTCCCAATTCTTCTAGAAAGATCCGTTGCGAAGAAAGAGAGATA 541
QY 160 ArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValIleThrAsnValGlyGly 179
Db 542 AGGTTTACCGTCAATGAGACACTCACTTCAACCTGCTTTTGATACAAATGTCGAGGA 601
QY 180 AlaGlyAspValHisSerValSerIleLysGlySerArgThrGlyTyrGlnSerMetSer 199
Db 602 GCAGAGATGTGACATTCAGTATCAATCAAGGTTCAAAAGACTGATGCAAGCAATGTCA 661
QY 200 ArgAsnTyrGlyGlnAsnTyrGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPhe 219
Db 662 AGGAAGTGGGGCCAAATTTGGCAGAGCAATCTTATCTTAAACGGCCAAAGTCTTTTC 721
QY 220 GlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTyr 239
Db 722 CAAGTGACAGCCAGTGACGCGAGACTGTGACTAGCAACAATGTTGTGCTGAATTTGG 781
QY 240 GlnPheGlyGlnThrTyrGluGlyProGlnPhe 250
Db 782 CAATTGGGCAAACTTTGAGGGGTGTCAGTTT 814

RESULT 2

CD575807 816 bp mRNA linear EST 12-JUN-2003
LOCUS UCRPT01_01ae06.g3 Poncirus trifoliata CTV-challenged cDNA library -
DEFINITION AGI Poncirus trifoliata cDNA clone UCRPT01_01ae06, mRNA sequence.

ACCESSION CD575807
VERSION CD575807.1 GI:31671709
KEYWORDS EST.
SOURCE Poncirus trifoliata
ORGANISM Poncirus trifoliata

REFERENCE 1 (bases 1 to 816)
AUTHORS Roose,M.L., Ye,X., Federici,C.F., Close,T.J., Fenton,R.D.,
TITLE Wanamaker,S., Collura,K., Feuerbacher,O., Kim,H.R., Kudrna,D., Wing
JOURNAL Development of EST Resources and New Genetic Markers for California
COMMENT Citrus - Poncirus trifoliata CTV-challenged phloem - AGI
Unpublished
Contact: Mikeal Roose
Department of Botany & Plant Sciences, University of California
Riverside, CA, 92521-0124, USA
Tel: 9097874137
Fax: 9097874437
Email: mikeal.roose@ucr.edu
Seq primer: T3.

FEATURES

Source

Location/Qualifiers

1. 816

/organism="Poncirus trifoliata"

/mol_type="mRNA"

/cultivar="Pomeroy OP"

/db_xref="taxon:37690"

/clone="UCRPT01.01ae06"

/tissue_type="Phloem"

/dev_stage="10 - 30 cm shoots"

/lab_host="E. coli TJC121"

/clone_lib="Poncirus trifoliata CTV-challenged cDNA library - AGI"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse at University of California, Riverside. The scion was a open-pollinated (very probably selfed) seedling of Poncirus trifoliata cv Pomeroy that was selected as homozygous for the Ctv resistance gene. The rootstock was sweet orange infected with citrus tristeza virus (CTV) isolate T514 over 1 year before sampling (CTV infects sweet orange, but not genotypes carrying the Ctv resistance gene. Shoots 10-30 cm long were harvested in October 2000, and the green phloem (bark) was removed and frozen quickly in dry ice. Total RNA was extracted using Trizol reagent (Gibco). Poly(A) RNA was purified, a cDNA library was made, and 0.5 million primary lambda cDNA clones were in vivo excised to give a population of Bluescript SK(-) phagemids. All steps to this point were performed in the M. Rouse lab at the University of California, Riverside by X. Ye. Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3730 at the Arizona Genomics Institute, University of Arizona (Collura, Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Wamamaker) using the Harvest pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."

BASE COUNT 210 a 196 c 195 g 215 t

ORIGIN

Alignment Scores:

Pred. No.: 7.82e-98 Length: 816

Score: 1153.50 Matches: 206

Percent Similarity: 90.65% Conservatave: 17

Best Local Similarity: 83.74% Mismatches: 22

Query Match: 82.75% Indels: 1

DB: 14 Gaps: 1

US-09-383-579c-10 (1-250) x CD575807 (1-816)

QY 1 MetAlaPheSerTyrSerProPheSerSerLeuPheLeuPhePheValPhe 20

DB 77 ATTGCAGCATCATCTAGTGTCTCTCTTTGTTGTGCTCAATTTTGTTCGTGC 136

QY 21 ThrPheAlaSPtyr---GlyGlyTyrPglnsrGlyHIsAlaThrPheTyrGlyGly 39

DB 137 ACATTGGAGACTATGTGTGGTGGCAAGTGCCATGCACTTCTATGAGGGGT 196

QY 40 AspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyr 59

DB 197 GATGCTTCGGCACAATGGGTGGTGTGTGATGCAATTTGTACAGCCAAAGCTAT 256

QY 60 GlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAngLyLeuSerCysGlyAla 79

DB 257 GGGACTAACACTGCACACTAGTACCGCTATTCACCAATGGCCCTAAGCTGTGTTCA 316

QY 80 CysPheGlnMetThrCysThrAsnAspProLySTrpCysLeuProGlyThrIleArgVal 99

DB 317 TGCTATGAATGAATGAAATGAAATGACCCCAAGTGTGCTCCCGGCTCCATCATTTGTC 376

QY 100 ThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAngLyGlyTyrCys 119

DB 377 ACCGCCACCAACTTCTGTGCCACCTAACCTTGCCCTGTCTTAACGACAAACGGCGTGTGC 436

QY 120 AsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyr 139

DB 437 AATCTCCCTCCACGACACTTTCATGATGGTGAAGCCCGCTTCTTGCACAAATGCCCAATAC 496

QY 140 ArgAlaGlyIleValProValSerPheArgArgValProCysMetLyLeuGlyGlyVal 159

DB 497 CGTGCCGGTATCGTCCCAATTTCTTCAGAGGATCCCGTGTGCGAAGAAAGAGGAAATA 556

QY 160 ArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyGly 179

DB 557 AGGTTACCGTCAATGAGCACTCATCTCAACCTGTTTGATCACAATGTCCGAGGA 616

QY 180 AlaGlyAspValHisSerValSerIleLyGlySerArgThrGlyTyrPglnsrMetSer 199

DB 617 GCAGAGATGTGCATTGATCAATCAATCAAGGTTCAAAAGACTGATGCAAGCAATGTCA 676

QY 200 ArgAsnTrpGlyGlnAsnTrpGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPhe 219

DB 677 AGGAAGTGGGCCCCAAATGGCAGAGCAATTTCTTATCTTAACGGCCAAAGTCTTCTTTC 736

QY 220 GlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrp 239

DB 737 CAAGTACAGCCAGTACGCGCAGAGCTGACTAGCAACAAATGTTGTGCTCGAAATTTGG 796

QY 240 GlnPheGlyGlnThrTyr 245

DB 797 CAATTGGGCCAAACCTTT 814

RESULT 3

CB291406 809 bp mRNA 'linear EST 28-FEB-2003

LOCUS UCRCS01_02dd11_g1 Washington Navel orange cold acclimated flavedo & albedo cDNA library Citrus sinensis cDNA clone UCRCS01_02dd11, mRNA sequence.

DEFINITION

ACCESSION CB291406

VERSION CB291406.1 GI:28616863

KEYWORDS EST.

SOURCE Citrus sinensis

ORGANISM Citrus sinensis

REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids 1 (bases 1 to 809)

AUTHORS Close,T.J., Collura,K., Fenton,R.D., Feuerbacher,O., Kim,H.R., Kudrna,D., Wamamaker,S., Wing,R. and Yu,Y.

TITLE Development of EST Resources and New Genetic Markers for California Citrus

JOURNAL Unpublished

COMMENT Contact: Timothy Close

Department of Botany & Plant Sciences, University of California

Riverside, CA, 92521-0124.

Tel: 9097873318

Fax: 9097874437

Email: timothy.close@ucr.edu

Seq primer: T3.

FEATURES

Source

1. 809

/organism="Citrus sinensis"

/mol_type="mRNA"

/cultivar="Washington Navel"

/db_xref="taxon:2711"

/clone="UCRCS01_02dd11"

/tissue_type="Rind containing flavedo and albedo"

/dev_stage="Mature fruit"

/lab_host="E. coli TJC121"

/clone_lib="Washington Navel orange cold acclimated flavedo & albedo cDNA library"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid;

Site 1: Ecori; Site 2: XhoI; Plants were grown in the field at University of California, Riverside Agricultural Operations since 1983. The scion was Washington Navel orange and the rootstock Carizzo Citrange. Tissue from mature fruit was harvested at mid-day in January 2002 during a cold spell, when pre-dawn temperatures were approximately -2 to 2 degree C. Approximately 2 cm median sections of the rind were excised in the field from several fruits, then wrapped in aluminum foil and frozen quickly in dry ice. Total RNA was extracted using a phenol extraction procedure described in J. Japanese Soc. Hort. Sci. (1996) 64:809-814. Poly(A) RNA was purified, a cDNA library was made, and 1 million primary lambda cDNA clones were in vivo excised to give a population of pBluescript SK(-) phagemids. All steps to this point were performed in the Tü Close lab at the University of California, Riverside (Fenton). Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3130 at the Arizona Genomics Institute, University of Arizona (Collura, Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Wamamaker) using the HarVEST pipeline (<http://harvest.ucr.edu>) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."

BASE COUNT 210 a 196 c 191 g 212 t
ORIGIN

Alignment Scores:

Pred. No.: 5.38e-97 Length: 809
Score: 1144.50 Matches: 204
Percent Similarity: 90.61% Conservative: 18
Best Local Similarity: 83.27% Mismatches: 22
Query Match: 82.10% Indels: 1
DB: 14 Gaps: 1

US-09-383-579C-10 (1-250) x CB291406 (1-809)

```

QY 1 MetAlaPheSerTyrSerProPheSerSerLeuPheLeuLeuProPhePheValPhe 20
Db 73 ATGCGACGATCATCTAGTGTGCTCTCTCTTTGTTGTGCTCAATTTTGTTCGTCG 132
QY 21 ThrPheAlaAspTyr---GlyGlyTrpGlnSerGlyHisAlaThrPheTyrGlyGly 39
Db 133 ACATTGGAGACTATGGTGGTGGTGGCAAGTGGCCATGCACTTCTATGGCGGGGT 192
QY 40 AspaIaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyr 59
Db 193 GATGCTCCGGCACATGGGTGGTGGTGGTATGGCAATTGTACAGCCAGGCTAT 252
QY 60 GlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAla 79
Db 253 GGGACTAAACACTGCATCACTCAGTACCGCTTATTCAACAATGGCCCTAAGCTGTGTTCA 312
QY 80 CysPheGluMetThrCysThrAsnAspProLysTrpCysLeuProGlyThrIleArgVal 99
Db 313 TGCCTGAATGAATGTGAATGTGAATGTGAATGTGAATGTGAATGTGAATGTGAAT 372
QY 100 ThrAlaThrAsnPheCysProProAsnAsnAlaLeuProAsnAsnAsnGlyGlyTyrCys 119
Db 373 ACCGCCAACCACTTCTGCCCACTAAGCTTGGCTTGTCAACGACACGCGGTTGGTGC 432
QY 120 AsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyr 139
Db 433 AATCTTCCCTCCAGCACTTTGACATGGCTGAGCCCGCTTCTTGCAAAATGGCCCAATAC 492
QY 140 ArgAlaGlyIleValProValSerPheArgArgValProCysMetLysLysGlyGlyVal 159
Db 493 CGCGCGGTATCGTCCCAATTTCTTCAAGAAAGATCCGCTGTGCGAAGAAAGAGGATA 552
QY 160 ArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyGly 179

```

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Db 553 AGGTTACCGTCATGACACTGCTACTTCAACCTGGTTTGATCAACAATGTCGAGGA 612
QY 180 AlaGlyAspValHisSerValSerIleLeuGlySerArgThrGlyTrpGlnSerMetSer 199
Db 613 GCAGAGATGTACTTCACTTCAATCAAGGTTCAAGACTGATGGCAAGCAATGTCA 672
QY 200 ArgAsnTrpGlyGlnAsnTrpGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPhe 219
Db 673 AGGAAGTGGGGCCAAATTTGGCAGAGCAATTTCTTACCGGCAAGTCTTCTTC 732
QY 220 GlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrp 239
Db 733 CAATTGACAGCCAGTGCAGGAGAGTGTGACTAGCAACAATGTTGCTGCAATGG 792
QY 240 GlnPheGlyGlnThr 244
Db 793 CAATTGGGCAACC 807

```

RESULT 4

CB980842 838 bp mRNA linear EST 01-MAY-2003
LOCUS CAB70003_IIR_A03 Cabernet Sauvignon Berry Post-Veraison - CAB7

DEFINITION

Vitis vinifera cDNA clone CAB70003_IIR_A03 3', mRNA sequence.

ACCESSION

CB980842 GI:30304048

VERSION

EST.

KEYWORDS

Vitis vinifera

SOURCE

Vitis vinifera

ORGANISM

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

REFERENCE

1 (bases 1 to 838)

AUTHORS

Goes da Silva, F., Tandolino, A., Lim, H., Baek, J., Jones, K. and Cook

TITLE

Expressed sequence tags from cabernet sauvignon berries at various developmental stages

JOURNAL

Unpublished

COMMENT

Contact: Douglas Cook, PhD

FEATURES

CAES Genome Facility

source

UC Davis, Plant Pathology

FEATURES

One Shields Ave, Davis, CA 95616, USA

source

Tel: 530 754 6561

source

Fax: 530 754 6617

source

Email: drcook@ucdavis.edu

source

Seq primer: GCCAAGCAATGCTCTAG.

source

Location/Qualifiers

source

1..838

source

/organism="Vitis vinifera"

source

/mol_type="mRNA"

source

/cultivar="Cabernet Sauvignon"

source

/db_xref="taxon:29760"

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/clone="CAB70003_IIR_A03"

source

/sex="Hermaphrodite"

source

/dev_stage="Post-Veraison, 18-19 brix"

source

/lab_host="DH5alpha"

source

/clone_lib="Cabernet Sauvignon Berry Post-Veraison - CAB7"

source

/note="Organ: Berry; Vector: pDNR; Site 1: SfiI; Site 2: SfiI; CAB7 is a cDNA library of Cabernet Sauvignon Clone 8 berries. Samples were collected post-veraison from field-grown vines during stage III of berry growth at 89 days after full bloom. Berries soluble solid concentration ranged between 18-19 brix. Sampled vines were located at the University of California, Davis, Experimental vineyard. cDNAs were made by oligo-dT priming and directly cloned. 5' and 3' adaptors were used in cloning as follows: 5'-AAGCACTGTATCAACGACAGAGTGGCCATTACGGCCGG-3' and 5'-ATTCTAGAGCGGCGGCGGCGGCGGCAATG-dT(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

BASE COUNT 192 a 233 c 219 g 194 t

ORIGIN

Alignment Scores:

Pred. No.: 2.26e-96 Length: 838
 Score: 1138.00 Matches: 201
 Percent Similarity: 87.40% Conservative: 21
 Best Local Similarity: 79.13% Mismatches: 28
 Query Match: 81.64% Indels: 4
 DB: 14 Gaps: 1

US-09-383-579C-10 (1-250) x CB980842 (1-838)

QY 1 MetalapheserTyrSerPropheserSerleuPheleuProphetheValphe 20
 DB 34 CTCTCAATGGCTACTGCAGCATTTCTCTATCTCTGCCCCCTTCTCTCTGCTA 93
 QY 21 -----ThrpheAlaaspTyrGlyTyrPglInserGlyHisAlaThrPheTyr 36
 DB 94 TGCCCTCCAGGACAAATGTTGCTATGTTGGGTGGAGGTGGCATGCCCATTTCTAT 153
 QY 37 GlyGlyGlyAspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSer 56
 DB 154 GCGCGTGTGACGCCCTCAGGACCAATGGGTGGGCTGTGGGTATGGCACTTGTAACAGC 213
 QY 57 GlnGlyTyrGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnGlyLeuSer 76
 DB 214 CAAGGATATGGACCAACACTGCAGCTCTCAGACCCGCTCTTCAACAGTGGGCTGAGC 273
 QY 77 CysGlyAlaCysPheGluMetThrCysThrAsnAspProlySerTyrCysLeuProGlyThr 96
 DB 274 TGTGGGGCATGTTACGAGATGAATGCAACGATGACCCCAATGTGTGCTCCAGGGAGCC 333
 QY 97 IleArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnGly 116
 DB 334 CTAACTGATGCTCCACAACTTCTGCCCTCTTAACCTTGCTTCCAAACACCAACGAGC 393
 QY 117 GlyTyrCysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIle 136
 DB 394 GGATGTGCAATCCGCCCTCTGAGCACTTGATCTAGCTGAGCTGCTTCTTCAAGATT 453
 QY 137 AlaGlnTyrArgAlaGlyIleValProValSerPheArgValProCysMetLysLys 156
 DB 454 GCCCAGTACCGAGCTGGAATCGTCTGTCTTTCAGAGAGTCCCTGTGTGAAGAAA 513
 QY 157 GlyGlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsn 176
 DB 514 GGAGGATCCGCTTTACATCAACGGCCACTCTCACTTCACTTGGTGTCTATCAACAAC 573
 QY 177 ValGlyGlyAlaGlyAspValHisSerValSerIleLysGlySerArgThrGlyTyrGln 196
 DB 574 GTGGCCGAGCGGAGAGACGTCAAGGCGCATATAGGGGTCTTAAGACCGGCTGGCAG 633
 QY 197 SerMetSerArgAsnTyrPglInserAsnTyrPglInserAsnTyrLeuAsnGlyGly 216
 DB 634 CCCATGTCAAGGAATGGGGCCAGAACTGGCAGAGCAACTCATCTCAACGGCCAGACC 693
 QY 217 LeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValPro 236
 DB 694 CTCTCATTCAGATCACAGCAAGCATGCGCGCATGACAGCCTCAATGTGGCGCCT 753
 QY 237 SerAsnTyrPglInPheGlyInThrTyrGlyGlyProGlnPhe 250
 DB 754 GCTGGCTGGCAGTTTGGGCAACATATGAGGGGCTCAGTTTC 795

RESULT 5
 LOCUS CB293003
 DEFINITION 799 bp mRNA linear EST 28-FEB-2003
 UCRCS01_05bf07_g1 Washington Navel orange cold acclimated flavedo & albedo cDNA library Citrus sinensis cDNA clone UCRCS01_05bf07, mRNA sequence.
 ACCESSION CB293003
 VERSION CB293003.1 GI:28618460
 KEYWORDS EST.
 SOURCE Citrus sinensis
 ORGANISM Citrus sinensis

REFERENCE
 AUTHORS Close,T.J., Collura,K., Fenton,R.D., Feuerbacher,O., Kim,H.R., Kudrna,D., Wanmaker,S., Wing,R. and Yu,Y.
 TITLE Development of EST Resources and New Genetic Markers for California Citrus
 JOURNAL Unpublished
 COMMENT Contact: Timothy Close
 Department of Botany & Plant Sciences, University of California
 Riverside, CA, 92521-0124
 Tel: 9097873318
 Fax: 9097874437
 Email: timothy.close@ucr.edu
 Seq primer: T3.

FEATURES
 source
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 /organism="Citrus sinensis"
 /mol_type="mRNA"
 /cultiivar="Washington Navel"
 /db_xref="taxon:2711"
 /clone="UCRCS01_05bf07"
 /tissue_type="Rind containing flavedo and albedo"
 /dev_stage="Mature fruit"
 /lab_host="E. coli TUC121"
 /clone_lib="Washington Navel orange cold acclimated flavedo & albedo cDNA library"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; Plants were grown in the field at University of California, Riverside Agricultural Operations since 1983. The scion was Washington Navel orange and the rootstock Carizzo Citrange. Tissue from mature fruit was harvested at mid-day in January 2002 during a cold spell, when pre-dawn temperatures were approximately -2 to 2 degree C. Approximately 2 cm median sections of the rind were excised in the field from several fruits, then wrapped in aluminum foil and frozen quickly in dry ice. Total RNA was extracted using a phenol extraction procedure described in J. Japanese Soc. Hort. Sci. (1996) 64:809-814. Poly(A) RNA was purified, a cDNA library was made, and 1 million primary lambda cDNA clones were in vivo excised to give a population of pluescript SK(-) phagemids. All steps to this point were performed in the TJ Close lab at the University of California, Riverside (Fenton). Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3530 at the Arizona Genomics Institute, University of Arizona (Collura, Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Wanmaker) using the HarVEST pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."

BASE COUNT 208 a 195 c 189 g 207 t
 ORIGIN

Alignment Scores:
 Pred. No.: 4.58e-96 Length: 799
 Score: 1134.50 Matches: 202
 Percent Similarity: 90.53% Conservative: 18
 Best Local Similarity: 83.13% Mismatches: 22
 Query Match: 81.38% Indels: 1
 DB: 14 Gaps: 1

US-09-383-579C-10 (1-250) x CB293003 (1-799)

QY 1 MetalapheserTyrSerPropheserSerleuPheleuProphetheValphe 20
 DB 69 ATTGACGATCATCTAGTGTGCTCTCTTTGTGTGCTCAATTTGCTTGTGCGC 128

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QY      21 ThrPheAlaAspTyr---GlyGlyTyrPglInserGlyHisAlaThrPheTyrGlyGly 39
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Db      129 ACATTGGAGACTATGTTGGTGGTGGCAAAAGTGGCATTGCAACTTCTATGCGGGGCT 188
QY      40 AspaIaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyr 59
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      189 GATGCTTCCGGCACAATGGGTGGTGGTGGTATGGCAATTTGTACAGCCAAAGGCTAT 248
QY      60 GlyThrAsnThrValAlaIeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAla 79
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      249 GGGACTAACACTGACGACTCAGTACCGCTCTATTCAACATGCGCTAAGCTGTGTTCA 308
QY      80 CysPheGluMetThrCysThrAsnaAspProLysTyrCysLeuProGlyThrIleArgVal 99
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      309 TGCTATGAATGAATGTGAATGTGAATGACCCCAAGTGTGCTCCCGGCTCCATCATGTGC 368
QY      100 ThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTyrCys 119
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      369 ACCGCCAACCACTTCTGCCCCACCTAAGCTTGTCTAACGACACGCGGTTGTTGC 428
QY      120 AsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyr 139
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      429 AATCTCCCTCCAGACTTGTGACATGCTGAGCCGCTTCTTGCAATGTCCTCAATAC 488
QY      140 ArgAlaGlyIleValProValSerPheArgArgValProCysMetLysGlyGlyVal 159
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      489 CGCGCCGGTATCGTCCCAATTCCTTACAGAGATCCCGTGTGCGAAGAAAGAGATA 548
QY      160 ArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyGly 179
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      549 AGGTTACCGTCAATGACACTCATCTTCAACCTGTTTGTATCAACAATGTGCGAGA 608
QY      180 AlaGlyAspValHisSerValSerIleLysGlySerArgThrGlyTyrPglInserMetSer 199
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Db      609 GCAGAGATGTACATTCAGTATCAATCAAGGTTCAAGAAGTGGATGGCAAGCAATGTCA 668
QY      200 ArgAsnTyrGlyGlnAsnTyrPglInserAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPhe 219
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      669 AGGAAGTGGGGCCAAATGCGACAGACCAATCTTATCTTAACGCCCAAGCTTCTTTC 728
QY      220 GlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTyr 239
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Db      729 CAATTGACAGCCAGTGCAGCGCAGACTGTGACTAGCAACAATGTTGTGCTGGAATTTGG 788
QY      240 GlnPheGly 242
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Db      789 CAATTGGGG 797

```

RESULT 6
 BG581975 798 bp mRNA linear EST 11-APR-2001
 LOCUS EST483712 GVN Medicago truncatula cdna clone pGVN-66124 5' end,
 DEFINITION mRNA sequence.
 ACCESSION BG581975
 VERSION BG581975.1 GI:13597039
 KEYWORDS EST.
 SOURCE Medicago truncatula (barrel medic)
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.
 1 (bases 1 to 798)
 REFERENCE
 AUTHORS Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Town
 ,C.D., Van Aken,S., Utebback,T., Cho,J. and Fraser,C.M.
 TITLE ESTs from one month old nitrogen-fixing root nodules of Medicago
 truncatula, 2001
 JOURNAL Unpublished
 COMMENT Contact: Carroll P. Vance
 Department of Agronomy and Plant Genetics
 University of Minnesota
 411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
 Tel: 612 625 5715

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FEATURES
  source
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      /organism="Medicago truncatula"
      /mol_type="mRNA"
      /cultivar="genotype A17"
      /db_xref="taxon:3880"
      /clone="pGVN-66124"
      /issue_type="N2-fixing root nodules"
      /dev_stage="effective root nodules harvested one month
      post inoculation with Sinorhizobium meliloti"
      /lab_host="E. coli strain XLOLR"
      /clone_lib="GVN"
      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
      XhoI; cDNA was prepared from polyA+ enriched RNA from
      effective root nodules harvested one month post
      inoculation with Sinorhizobium meliloti. The cDNA was
      directionally ligated into the Uni-ZAP XR vector from
      StrataGene and packaged using Gigapack III Gold packaging
      extracts. Plasmids containing cDNA inserts were excised
      from the recombinant lambda-ZAP phage using Ex-Assist
      helper phage and propagated in XLOLR cells."
BASE COUNT  221 a  173 c  175 g  229 t
ORIGIN
Alignment Scores:
Pred. No.:      4.89e-95      length: 798
Score:          1123.50      matches: 200
Percent Similarity: 89.02%      Conservative: 19
Best Local Similarity: 81.30%      Mismatches: 24
Query Match:    80.60%      Indels: 3
DB:              10      Gaps: 2
US-09-383-579C-10 (1-250) x BG581975 (1-798)
QY      1 MetaIaPheSerTyrSerProPheSerSerLeu-----PheLeuLeuProPhePhe 18
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      60 ATGGCAATAGTAGCAACTCATATCATCTCTATTTCTTGTGTTCTTAGCTTATGCTT 119
QY      19 ValPheThrPheAlaAspTyr--GlyGlyTyrPglInserGlyHisAlaThrPheTyrGly 37
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      120 AGAGCACTTTTGTGACTATGAGGTGAGTGGAAATGCCATGCCACATTTATGCT 179
QY      38 GlyIaAspaIaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGln 57
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Db      180 GGAGGAGATGATCAGCAGCAACATGGAGGGCTTGTGTTATGAAATTTGTATAGCCAA 239
QY      58 GlyTyrGlyThrAsnThrValAlaIeuSerThrAlaLeuPheAsnAsnGlyLeuSerCys 77
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Db      240 GGCTATGGAACCAACACTGCTGCACTAAGCACCTGCTTTCAACAATGATTGAGTTGT 299
QY      78 GlyIaCysPheGluMetThrCysThrAsnaAspProLysTyrCysLeuProGlyThrIle 97
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Db      300 GGGTCTTGCTACGAGATGAATGTACAGATGACCTTAATGTGTGCTTCTGTAGCATTA 359
QY      98 ArgValThrAlaThrAsnPheCysBProAsnPheAlaLeuProAsnAsnAsnGlyGly 117
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Db      360 TTGGTACTGTCTACAACTTCTGCCCCCAAACTTGCAGAGTCTAATACCAATGTGGA 419
QY      118 TyrCysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAla 137
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      420 TGGTGAAACCTCCCTTCAGACACTTGTATCTTGTGAGCCTGCTTCTTACAAATGCT 479
QY      138 GlnTyrArgAlaGlyIleValProValSerPheArgArgValProCysMetLysGlyGly 157
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      480 CAATACAAAGCTGGAATGTTCTCTATTCTTCAAGAAAGTCCCGCTATGAAGAAAGA 539
QY      158 GlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnVal 177
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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Db 540 GGAATCAGATTCAATMAATGACACTCATACTTCAACTTGGTTTGGTCACAAATGTT 599

Qy 178 G1YGLYALAGIYASPVAlHiservalSerlelySGlySerArgThrgLYTPGInSer 197
|||||
Db 600 GGTGAGCTGAGATGTACATCTGTGTCCATCAAGGATCAAGAAGCTGATGGCAAGCT 659

Qy 198 MetSerArgAsnTrpGLYInAsnTrpGLInSerAsnTyrLeuAsnGLYInGLYLeu 217
|||||
Db 660 ATGTCTAGGAAGCTGGGGCAGAACTGGCAAGCAATACTATCTCAATGTCGAAGCCTC 719

Qy 218 SerPheGLInValThrLeuSerAspGLYArgThrLeuThrAlaTyrAsnLeuValProSer 237
|||||
Db 720 TCATTCCAAGTCACTACAAGTATGTAGAACTATCACTAGCAACAACGTTGTGCTGGC 779

Qy 238 AsnTrpGLInPheGLYIn 243
|||||

Db 780 AATTGGCAATTGGACAG 797

RESULT 7

CD486517

LOCUS 736 bp mRNA linear EST 04-JUN-2003
DEFINITION CRH3.3F02 Cotton Root and Hypocotyl Lambda ZIPLOX Library (CRH)
Gossypium hirsutum cDNA clone CRH3.3F02 5' similar to expansin,
mRNA sequence.

ACCESSION

CD486517

VERSION CD486517.1 GI:31407482

KEYWORDS

EST.

SOURCE Gossypium hirsutum (upland cotton)

ORGANISM Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosidsREFERENCE 1 (bases 1 to 736)
Dowd,C., Wilson,I. and McFadden,H.AUTHORS Different Gene Expression Responses in Cotton Root and Hypocotyl
TITLES tissues during infection with Fusarium Wilt Disease

JOURNAL Unpublished (2003)

COMMENT Contact: Caltriona Dowd, Helen McFadden
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry
Black Mountain Laboratories, Cnr Clunies Ross Street & Barry Drive,
Black Mountain, Canberra, ACT, 2601, Australia
Tel: 61 2 6246 4914, 6246 5377
Fax: 61 2 6246 5000
Email: Caltriona.Dowd@csiro.au, Helen.McFadden@csiro.au
Vector clipped sequences Bases 1-17 (GTCGCCACCGCTCCG): SalIFEATURES
Source
1. .736
/organism="Gossypium hirsutum"
/mol_type="mRNA"
/cultivar="DeltaEMERALD"
/db_xref="taxon:3635"
/clone="CRH3.3F02"
/tissue_type="Root and hypocotyl tissues"
/dev_stage="5 day old seedlings"
/lab_host="Y1090(ZL)"
/clone_lib="Cotton Root and Hypocotyl Lambda ZIPLOX
Library (CRH)"
/note="Vector: Lambda ZIPLOX; Site_1: SalI; Site_2: NotI;
mRNA was prepared from root and hypocotyl tissues of the
cotton cultivar DeltaEMERALD. cDNA was synthesised from a
NotI-oligoDT primer/adaptor using the manufacturers
protocols (Life Technologies) and then ligated to a SalI
adaptor to facilitate directional cloning. The cDNA was
cloned into the SalI and NotI sites of the Lambda ZIPLOX
phage vector (Life Technologies). Constructed by Caltriona
Dowd and Helen McFadden."BASE COUNT 182 a 188 c 176 g 190 t
ORIGIN

Alignment Scores:

Pred. No.:	6.36e-93	Length:	736
Score:	1100.50	Matches:	198
Percent Similarity:	90.60%	Conservative:	14
Best Local Similarity:	84.62%	Mismatches:	17
Query Match:	78.95%	Indels:	5
DB:	14	Gaps:	2

US-09-383-579c-10 (1-250) x CD486517 (1-736)

Qy 6 SerProPheSerSer-----LeuPheLeuLeuProPhePheValPheThr 21
|||||
Db 33 TCACCATTTTCTACTACTTCTCTTATCTCTTCATCTCACTTTTACCCTGACAACACC 92

Qy 22 PheAlaAspTyr--GlyGLYTrpGLInSerGLYHisAlaThrPheTyrGLYGLYAsp 40
|||||

Db 93 ATTGGTACTATGGTGGAGATGGCAAGGTGTACGCCACCTTCTACGGCGGTGTGAT 152

Qy 41 AlaSerGLYThrMetGLYGLYAlaCysGLYTYrGLYAsnLeuTYrSerGLNGLYTYrGLY 60
|||||

Db 153 GCATCCGGCACAATGGAGAGTGTGTGTGATATGTAATTAATAGCAAGGTTTGGG 212

Qy 61 ThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGLYLeuSerCysGLYAlaCys 80
|||||

Db 213 ACCAACACAGCAGCAGCTTACACTGATGTTCAACAATGGGTTGAGCTGTGTTCTTGT 272

Qy 81 PheGLUmetThrCysThrAsnAspProLYsTrpCysLeuProGLYThrIleArgValThr 100
:::|||||

Db 273 TATGAATAGAGGTGTGATGTGACCCAAATAGTGCTTGCCTTACCATTAATGTGCTACT 332

Qy 101 AlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGLYTYrCysAsn 120
|||||

Db 333 GCCACCAATTTTGTGTCCTTAATTTGCTTTGTCCAAATGATATATGTTGGTGTGCAAC 392

Qy 121 ProProLeuGLNHisPheAspMetAlaGLUProAlaPheLeuGLNleAlaGLNTrpArg 140
|||||

Db 393 CTTCCATTGCAACACTTGTATTTGGCCGAGCTGCTTTTGGCAATAGCTCAATACCGT 452

Qy 141 AlaGLYIleValProValSerPheArgValProCysMetLYsLYsGLYValAlaArg 160
|||||

Db 453 GCTGGATTGTACCCGTTTCATTTCAGAGAGTCCCATGTATAAAGAAAGAGAGTCCGA 512

Qy 161 PheThrIleAsnGLYHisSerTyrPheAsnLeuValLeuIleThrAsnValGLYAla 180
|||||

Db 513 TTCACAATCAACGGCCACTCATCTTCACTTGTCTTAATCACTAACGTTGGCGCGCC 572

Qy 181 G1YASPVAlHiservalSerlelySGlySerArgThrgLYTPGInSerMetSerArg 200
|||||

Db 573 GGAGATGTCCACTCGGTGTCATCAAGGCTCGAAACTGGGTGGCAAGCAATGTCAAGG 632

Qy 201 AsnTrpGLYInAsnTrpGLInSerAsnAsnTyrLeuAsnGLYInGLYLeuSerPheGLN 220
|||||

Db 633 AACTGGGGCAGAACTGGCAGAACCACTAACCCTCAACGCCCAACCCCTCTTCCAA 692

Qy 221 ValThrLeuSerAspGLYArgThrLeuThrAlaTyrAsnLeu 234
|||||

Db 693 GTCACACACAGCGATGGCAAGACTTAACCAAGCTACAACGTC 734

RESULT 8

CB980777

LOCUS 772 bp mRNA linear EST 01-MAY-2003
DEFINITION CAB70003_riaf_A03 Cabernet Sauvignon Berry Post-Veraison - CAB7
Vitis vinifera cDNA clone CAB70003_riaf_A03 5', mRNA sequence.

ACCESSION CB980777

VERSION CB980777.1 GI:30303983

KEYWORDS EST.

SOURCE Vitis vinifera

ORGANISM Vitis vinifera

REFERENCE 1 (bases 1 to 772)
Goes da Silva,F., Tandolino,A., Lim,H., Baek,J., Jones,K. and Cook

during a cold spell, when pre-dawn temperatures were approximately -2 to 2 degree C. Approximately 2 cm median sections of the rind were excised in the field from several fruits, then wrapped in aluminum foil and frozen quickly in dry ice. Total RNA was extracted using a phenol extraction procedure described in J. Japanese Soc. Hort. Sci. (1996) 64:809-814. Poly(A) RNA was purified, a cDNA library was made, and 1 million primary lambda cDNA clones were in vivo excised to give a population of plasmid SK(-) phagemids. All steps to this point were performed in the TJ Close lab at the University of California, Riverside (Fenton). Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3530 at the Arizona Genomics Institute, University of Arizona (Collura, Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Wanamaker) using the Harvester pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."

BASE COUNT 202 a 199 c 186 g 201 t
ORIGIN

Alignment Scores:
Pred. No.: 1.3e-92 length: 788
Score: 1097.50 Matches: 197
Percent Similarity: 90.30% Conservative: 17
Best Local Similarity: 83.12% Mismatches: 22
Query Match: 78.73% Indels: 1
DB: 14 Gaps: 1

US-09-383-579c-10 (1-250) x CB290960 (1-788)

Oy 1 MetAlaPheSerTyrSerProPheSerSerLeuPheLeuProPhePheValPhe 20
Db 76 ATTGCAGCATCATCTAGCGTCTCTCTTTGTTGTGCTCAATTTTGTTCGTGC 135
Oy 21 ThrPheAlaAspTyr--GlyGlyTyrGlnSerGlyHisAlaThrPheTyrGlyGly 39
Db 136 ACATTGGAGACTATGTGTGGGTGGCAAGTGGCCATGCACTTCTATGGCGGGGT 195
Oy 40 AspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyr 59
Db 196 GATGCTTCGGGCAATGAGGTGGTGTGTGGGTATGCAATTTGTACAGCCAGGCTAT 255
Oy 60 GlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAla 79
Db 256 GGGACTAACTGACGACACTAGTACCGCTCTATTCACACATGGCCCTAGCTGTGATCA 315
Oy 80 CysPheGluMetThrCysThrAsnAspProLysTyrCysLeuProGlyThrIleArgVal 99
Db 316 TGCTATGAATGAATGTAATAATGACCCCAAGTGTGCTCCCGGCTCCATCATTTGTC 375
Oy 100 ThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTyrCys 119
Db 376 ACCGCCACCACTTCTGCCCACTTAACCTTGCCCTGTCTAACGACACGCGGTTGTGTC 435
Oy 120 AsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyr 139
Db 436 AATCCTCCCTCCAGACCTTGAACATGGCTGAGCCCGCTTCTTGAATTTGCCCAATAC 495
Oy 140 ArgAlaGlyIleValProValSerPheArgValProCysMetIleGlyGlyVal 159
Db 496 CGCGCCGCGATCGTCCCAATTTCTTCAAGAGATCCCGTGTGCCAAGAAAGAGGAATA 555
Oy 160 ArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyGly 179
Db 556 AGGTTTACCGTCAATGACACTCATCTTCAACTGTGTTGGTACAAATGTGGAAGA 615
Oy 180 AlaGlyAspValHisSerValSerIleGlySerArgThrGlyTyrGlnSerMetSer 199

Db 616 GCACGAGATGTACATTCAATCAAGGTTCAAGACTGATGCAAGCAATGTCA 675
Oy 200 ArgAsnTyrGlyGlnAsnTyrGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPhe 219
Db 676 AGGAAGTGGGGCAAAATGGCAGAGCAATCTTATCTTAACGCCCAAGTCTTCTTTC 735
Oy 220 GlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValPro 236
Db 736 CAAGTACAGCAGCAGTACGCGGAGGAGTGTGACTAGCAACAATGTGTGCTT 786

RESULT 10
BI932999

LOCUS BI932999 767 bp mRNA linear EST 18-OCT-2001
DEFINITION EST552888 tomato flower, 8 mm to preanthesis buds Lycopersicon
esculentum cDNA clone CTC24J22 5' end, mRNA sequence.

ACCESSION BI932999
VERSION BI932999.1 GI:16247471
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 767)

AUTHORS van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J.,
Utecherback, T., Van Aken, S., Romning, C.M., Nierman, W., Fraser, C.M.,
Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.

TITLE Generation of ESTs from tomato flower tissue, buds 8 mm -
preanthesis
JOURNAL Unpublished
COMMENT Contact: CUGI
Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.

FEATURES
source Location/Qualifiers

1..767
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CTC24J22"
/tissue_type="flower"
/dev_stage="buds 8mm to preanthesis"
/clone_lib="tomato flower, 8 mm to preanthesis buds"
/note="Vector: pBluescript SK(-); Site_1: SCORI, Site_2:
XhoI; supplier: Cornell University; Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."

BASE COUNT 215 a 144 c 168 g 240 t
ORIGIN

Alignment Scores:
Pred. No.: 4.43e-91 length: 767
Score: 1081.00 Matches: 188
Percent Similarity: 88.94% Conservative: 21
Best Local Similarity: 80.00% Mismatches: 26
Query Match: 77.55% Indels: 0
DB: 12 Gaps: 0

US-09-383-579c-10 (1-250) x BI932999 (1-767)

Oy 16 PhePhePheValPheThrPheAlaAspTyrGlyTyrGlnSerGlyHisAlaThrPhe 35
Db 5 TTTGCTTCTATTCTTTGCTGATATGAGGATGGCAAACTGCTCATGCACTTTC 64
Oy 36 TyrGlyGlyGlyAspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyr 55

Db 65 TATGAGGGGGTGATGCTCTGCGACAATGGGGGCTTGTGATATGAAATTGTAT 124

QY 56 SerGInGlyTyrGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAnglyLeu 75
|||||
Db 125 AGCCAAAGGATGATGAACTAACACTGCAGCACTAAGTACAGCACTATTCACAATGGTTTA 184

QY 76 SerCysGlyAlaCysPheGluMetThrCysThrAsnAspProLyserTrpCysLeuProGly 95
:::|||||
Db 185 ACTGTGTGCTGTGTATGAGCTCACTGCAACAATGCAGCTCAATGGTGTCTCCAAAGG 244

QY 96 ThrIleArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsn 115
|||||
Db 245 ACTATTACTGTCACTGCAACTAATTGTTGTCCTCGAAACCGCTCTCTAACCCTAACATAAT 304

QY 116 GlyGlyTrpCysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGln 135
|||||
Db 305 GGTGTTGTGTCGAATCCTCTCTCCACATTTGATTTAGCACAACTGCTTCTTGCAA 364

QY 136 IleAlaGlnTyrArgAlaGlyIleValProValSerPheArgValProCysMetIys 155
|||||
Db 365 ATGCTAAATACAAAGCCGGTATCGTCCCTGATCTTTTGAAGGGTCCCTGTATGAGA 424

QY 156 LysGlyGlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThr 175
|||||
Db 425 AAAGGAGGAATAAGGTTTACAGTAAATGAGACACTCTTTTCAACTGGTTTATGACACA 484

QY 176 AsnValGlyGlyAlaGlyAspValHisSerValSerIleIysGlySerArgThrGlyTrp 195
|||||
Db 485 AATGTTGAGAGTGCTGTGATATTCATCATCAGTTCAATTAAGGGTCTAATACTGATGG 544

QY 196 GlnSerMetSerArgAsnTrpGlyGlnAsnTrpGlnSerAsnAsnTrpLeuAsnGlyGln 215
|||||
Db 545 CAAGCATGTCAAGATATTGGGGCCAAATTTGGCAAGCAATTCTAATCTATATGTCGA 604

QY 216 GlyLeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuVal 235
|||||
Db 605 AGCTTTCATTTTCATGTCACACACAGATGAGAGACACTCATTAGCAACAATGCTGCA 664

QY 236 ProSerAsnTrpGlnPheGlyGlnThrTyrGluGlyProGlnPhe 250
|||||
Db 665 CCAATAATTTGGCAATTTTGACACACTTTTGAAGGGGCTCAATTT 709

RESULT 11
CB822230 864 bp mRNA linear EST 16-MAY-2003
LOCUS CB822230
DEFINITION EST 3081 Half-Ripe Apricot Fruit Lambda Zap II Library Prunus
armeniaca cDNA clone be005k06 3', mRNA sequence.
ACCESSION CB822230
VERSION CB822230.1 GI:29956247
KEYWORDS EST.
SOURCE Prunus armeniaca (apricot)
ORGANISM Prunus armeniaca
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
REFERENCE 1 (bases 1 to 864)
AUTHORS Grimpel,J., Romieu,C., Audergon,J.M., Albagnac,G., Lambert,P.,
Bouchet,J.P. and Terrier,N.
TITLE High Throughput Detection of Isogenes among 5724 3' EST from
Apricot Fruit(Prunus armeniaca)
JOURNAL Unpublished
COMMENT Contact: Audergon JM
Unite de genetique et amelioration des fruits et legumes
Institut National de la Recherche Agronomique
Domaine Saint-Maurice BP 94 84143 Montfavet cedex
Tel: 00-33-(0)4-32-72-26-68
Fax: 00-33-(0)4-32-72-26-62
Email: audergon@avignon.inra.fr
Seq primer: T7.

FEATURES
Source location/Qualifiers
1..864
/organism="Prunus armeniaca"
/mol_type="mRNA"

/cultivar="Bergeron"
/db_xref="taxon:36596"
/clone="be005k06"
/dev_stage="Half-Ripe stage"
/clone_1ib="Half-Ripe Apricot Fruit Lambda Zap II Library"
/note="Organ: Fruit; Vector: Lambda Zap II; Site_1: Eco RI
; Site 2: XhoI; Oriented library, construction described
in Molecular cloning and expression of a cDNA encoding
1-aminocyclopropane-1-carboxylate (ACC) oxidase from
apricot fruit (Prunus armeniaca cv. Bergeron) by
Mbeguie-Mbeguie D, Chahine H, Gomez RM, Gouble B, Audergon
JM, Souty M, Albagnac G, Fils-Lycaon B in Physiol Plant
105:294-303 1999"

BASE COUNT 215 a 209 c 200 g 238 t 2 others
ORIGIN

Alignment Scores:
Pred. No.: 9.58e-91 Length: 864
Score: 1078.00 Matches: 200
Percent Similarity: 88.14% Conservative: 23
Best Local Similarity: 79.05% Mismatches: 26
Query Match: 77.33% Indels: 5
DB: 14 Gaps: 4

US-09-383-579c-10 (1-250) x CB822230 (1-864)

QY 1 MetAlaPhe---SerTyrSerProPheSerLeuPhe---LeuLeuProPhePhe 18
|||||
Db 77 ATGCTTTTACCTACCACTTAGCCATGCTCTTCTGTCTCTGTTCTCAATCTATGCTT 136

QY 19 ValPheThrPheAlaAspTyr---GlyGlyTrpGlnSerGlyHisAlaThrPheTyrGly 37
|||||
Db 137 CAAGCACTTATGGTGAATGATGAGAGAGATGGGAAGTGTCATGCCACATTATATGCT 196

QY 38 GlyGlyAspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGln 57
|||||
Db 197 GGGGTGATGCTCTGCGACAAATGGAGAGTGCTGTGATATGAAATTTGTATAGCAA 256

QY 58 GlyTyrGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAnglyLeuSerCys 77
|||||
Db 257 GGGTATGGAACCAACACTGCAGCTCTCAGCACAGCTCTGTTCAACGATGGCTGAGCTGT 316

QY 78 GlyAlaCysPheGluMetThrCysThrAsnAspProLyserTrpCysLeuProGlyThrIle 97
|||||
Db 317 GGGTCTTGTATGATGATGATGACAGTGAACCCCAATGTGCTCCCGGCAGCATC 376

QY 98 ArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAnglyGly 117
|||||
Db 377 ATGTCACCTGCCACAACTTCTGCCCTCTAAGCTCAGTCTAATGACAAATGTGGC 436

QY 118 TrpCysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAla 137
|||||
Db 437 TGTGCAACCTCTCTCCAGCACATTGATTGGCTGAGCCTGCTTTCACAAATGCT 496

QY 138 GlnTyrArgAlaGlyIleValProValSerPheArgValProCysMetIysGlyGly 157
|||||
Db 497 CAATACCGAGCTGGAATTGTCCCACTCTCTTCAAGAGGTTTCTGTGTGAAAAAGGA 556

QY 158 GlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnVal 177
|||||
Db 557 GGGATAGATTCAACCATCAACGCTCACTTACTTCAACTTGTTGATCACAACGTT 616

QY 178 GlyGlyAlaGlyAspValHisSerValSerIleIysGlySerArgThrGlyTrpGlnSer 197
|||||
Db 617 GGAGGTGCAAGGATGTGCACTCTGTTTCATCAACAGGGGTCCAAACAGGGTGGCAAGCC 676

QY 198 MetSerArgAsnTrpGlyGlnAsnTrpGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeu 217
|||||
Db 677 ATGTCAAGGAAGTGGGGCCAGAACTGCGAGAGTAAGTCTTACCTCAATGGCCAGGCTCTA 736

QY 218 SerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSer 237
|||||
Db 737 TC-TTTCAGTCAACCAACAGTGAACGTAAGAACTGTGACCAAGC---AATGCTGTGCCAGCT 792

QY 238 AsnTrpGlnPheGlyGlnThrTyrglyProGlnPhe 250
 Db 793 GACTGGCAGTTTGGTCAACATTTTCNGCGGTCAATTC 831

RESULT 12
 CD484188 681 bp mRNA linear EST 04-JUN-2003
 LOCUS atr01-4msl-d02 Atrol Amborella trichopoda cDNA clone atr01-4msl-d02
 DEFINITION 5', mRNA sequence.
 ACCESSION CD484188 GI:31405456
 VERSION CD484188.1 GI:31405456
 KEYWORDS EST.
 SOURCE Amborella trichopoda
 ORGANISM Amborella trichopoda
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; stem Magnoliophyta; Amborellaceae;
 Amborella.
 REFERENCE 1 (bases 1 to 681)
 AUTHORS depamphilis,C., Soltis,D., Soltis,P., Farmerie,W., Ma,H., Tanksley
 ,S., Leebens-Mack,J., Field,D., Buzgo,M., Kim,S., Ilut,D., Landherr
 ,L., Hu,Y., Wall,K., Albert,V., Carlson,J., Doyle,J., Frohlich,M.,
 Miller,W., Oppenheimer,D. and Theissen,G.
 TITLE Generation of ESTs from early flower buds of Amborella trichopoda
 JOURNAL Unpublished
 COMMENT Contact: Claude depamphilis or James Leebens-Mack
 Mueller Laboratory
 Penn State University
 208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
 State University, University Park, PA 16802, USA
 Tel: 814 863 6413
 Fax: 814 865 9131
 Email: cwd3@psu.edu or jhl10@psu.edu
 The sequence provided is trimmed of vector and low quality regions.
 Full sequence and original trace file are available from the Plant
 Genome Network website (http://pgn.cornell.edu)
 Plate: atr01-4msl row: d column: 02
 Seq primer: M13F.

FEATURES
 Location/Qualifiers
 1..681
 /organism="Amborella trichopoda"
 /mol_type="mRNA"
 /db_xref="taxon:13333"
 /clone="atr01-4msl-d02"
 /tissue_type="flower buds"
 /dev_stage="<= 2.5mm buds"
 /lab_host="SOLR"
 /clone_lib="Atrol1"
 /note="Vector: Bluescript SK (+/-); Site 1: EcoRI;
 Site 2: XhoI; Amborella trichopoda Baill; This library was
 made from male flowers only. Only floral buds with
 diameter of 2.5 mm or less were used for RNA isolation.
 This is a directionally cloned, non-normalized library.
 Avg. insert length: 1611; Primers: M13F and M13R;
 Antibiotic: 50 ug/ml Ampicillin; Primary Titer: 2.24E6 pfu
 total; Amplified Titer: 1.37E10 pfu/ml; Mass Excised
 Titer: 3.53E9 total; This library has been generated by
 the Floral Genome Project (FGP). We would like to thank
 David Lorence at the National Tropical Botanical Garden
 for providing plant material for library building. The
 Floral Genome Project is funded by NSF's Plant Genome
 Research Program (DBI-0115684). More information about the
 project can be obtained at http://feg.bio.psu.edu"

BASE COUNT 158 a 176 c 184 g 163 t

ORIGIN

Alignment Scores:
 Pred. No.: 3.75e-90 Length: 681
 Score: 1070.50 Matches: 188
 Percent Similarity: 92.86% Conservative: 20
 Best Local Similarity: 83.93% Mismatches: 15
 Query Match: 76.79% Indels: 2
 DB: 14 Gaps: 1

US-09-383-579c-10 (1-250) x CD484188 (1-681)

QY 22 PheAlaSerTyrglyGlyTrpGlnSerGlyHisAlaThrPheTyrglyGlyAspAla 41
 Db 9 TTGGAGACTAT--GGATGGCAGGC-GGCATGCCACATTTATGGTGGTGATGCT 64

QY 42 SerGlyThrMetGlyGlyAlaCysGlyTyrglyAsnLeuTyrsGlnGlyTyrglyThr 61
 Db 65 ACGGGACTATGGGGGAGCATGTGATATGGAACTGTATAGCCAAAGCTATGGCAGC 124

QY 62 AsnThrValAlaLeuSerThrAlaLeuPheAsnGlyLeuSerCysGlyAlaCysPhe 81
 Db 125 AACACAGACGCCCTGAGCACTGCTCTTCAACGATGGCTTGTGCTGCTAT 184

QY 82 GluMetThrCysThrAsnAspProLysTyrglyCysLeuProGlyThrIleArgValThrAla 101
 Db 185 GAAATGAGGTGCAATGACGACCCAAAGGTGGCTTCCAGGCTCCATTTGTCACTGCA 244

QY 102 ThrAsnProCysProProAsnPheAlaLeuProAsnAsnGlyGlyTyrglyAsnPro 121
 Db 245 ACCAATTCTGCCCCCAAAATTTGGTTGTCAAAATGACAAATGGTGGTGCACCC 304

QY 122 ProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrglyAla 141
 Db 305 CCTCTGCAACATTTTGACCTTGCTGTAACCTGCTTCCGCAAAATGCTGACAGGCT 364

QY 142 GlyIleValProValSerPheArgArgValProCysMetLysGlyGlyValArgPhe 161
 Db 365 GGAATTGGCTTGTGGCTTTAGAAGATACCTGTGTGAAGAAAGTGAATAAGTTTC 424

QY 162 ThrIleAsnGlyHisSerTyrglyPheAsnLeuValIleThrAsnValGlyAlaGly 181
 Db 425 ACCATCAATGGCCACTCCTCACTTCACTGCTCATATACTATAGTAGGCGCCGCT 484

QY 182 AspValHisSerValSerIleLysGlySerArgThrGlyTrpGlnSerMetSerArgAsn 201
 Db 485 GACATCCAGCGCGGTGTCCATCAAGGATCAACAGGTGATGGCAGCCCATGTCCAGAAC 544

QY 202 TrpGlyGlnAsnTrpGlnSerAsnAsnTyrglyLeuAsnGlyGlnGlyLeuSerPheGlnVal 221
 Db 545 TGGGGCCAAACTGGCAGACCACTCCTCACTCAATGAGCAGACCTCTCTCCAGTA 604

QY 222 ThrLeuSerAspGlyArgThrLeuThrAlaTyrglyAsnLeuValProSerAsnTrpGlnPhe 241
 Db 605 ACCACCACTGACGGCGCCGACCTCAACAGTTTCAACGTTGCCCTTCCAAATGGCAGTTTC 664

QY 242 GlyGlnThrTyrgly 245
 Db 665 GGCCAACTTTC 676

RESULT 13
 BE131139 815 bp mRNA linear EST 20-FEB-2001
 LOCUS L48-1090T3 Ice plant lambda Uni-Zap XR expression library, 48 hours
 DEFINITION NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-1090
 5', mRNA sequence.

ACCESSION BE131139
 VERSION BE131139.1 GI:8578502
 KEYWORDS EST.
 SOURCE Mesembryanthemum crystallinum (common iceplant)
 ORGANISM Mesembryanthemum crystallinum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Alzaceae; Mesembryanthemum.
 REFERENCE 1 (bases 1 to 815)
 Cushman, J.C.
 TITLE An expressed sequence tag database for the common ice plant,
 Mesembryanthemum crystallinum
 JOURNAL Unpublished
 COMMENT Contact: Cushman JC
 Department of Biochemistry
 University of Nevada

MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

PCR Primers
FORWARD: T7
BACKWARD: T3

Plate: L48-11 row: H column: 6
Seq primer: T3
High quality sequence stop: 350
POLYA=No.

FEATURES

source

1. 815
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="L48-1090"
/tissue_type="Leaf, 48 h 0.4M NaCl"
/dev_stage="Six week old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library
, 48 hours NaCl treatment"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI"

BASE COUNT 202 a 214 c 188 g 211 t
ORIGIN

Alignment Scores:

Pred. No.: 3.51e-89 Length: 815
Score: 1061.00 Matches: 196
Percent Similarity: 87.70% Conservative: 25
Best Local Similarity: 77.78% Mismatches: 29
Query Match: 76.11% Indels: 4
DB: 10 Gaps: 1

US-09-383-579c-10 (1-250) x BE131139 (1-815)

QY 1 MetAlaPheSerTyrSerProPheSerSerLeuPheLeuLeuProPhePheValPhe 20
Db 24 ATGGCCTTCTCAGCCATTTCAGTAGCTCCCTCTTCATCGCTTCATCTATGCCTT 83
QY 21 -----ThrPheAlaAspTyrGlyGlyTyrGlnSerGlyHisAlaThrPheTyrGlyGly 38
Db 84 CGCGGCGCATACGGCTATGAGGTGGTGGTCTAATGCTCATGCCACATTTTACGGTGA 143
QY 39 GLAAPAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGly 58
Db 144 GGGGAGCGCTCCGGCACTATGGGGGGTCTGTGATACGGAACCTGTACAGCCAGGG 203
QY 59 TyrGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGly 78
Db 204 TACGGAGCTAACACCGCGGCTTAAGCAGCGCCCTTCATATAACGGGTGAGCTGTGA 263
QY 79 AlaCysPheGluMetThrCysThrAsnAspProLysTyrCysLeuProGlyThrIleArg 98
Db 264 GCTTGCTATGAATGAATGTAACGACGACCCAGATGTGCAACCCAGAGCATTATA 323
QY 99 ValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTyr 118
Db 324 GTCACTGCTACCAATTCTGCCACCACTTAATTGCTTGGCTAACACCAATGTGGGTGG 383
QY 119 CysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGln 138
Db 384 TGCAACCTCTCTCTTCAGCACTTTCACATGGCTCAACCTGCTTTTGAAGATTGCCCAA 443
QY 139 TyrArgAlaGlyIleValProValSerPheArgArgValProCysMetLysGlyGly 158
Db 444 TACAAGCTGGAATAGTCCCTATTGCTTCAGAAAGGTACCTGTATGAGGAAGGTGA 503
QY 159 ValArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGly 178
Db 504 ATAAGGTTCAATAAAGGACACCTCTCACTTCAACCTCGTCTCATCTCCAAAGTTGGT 563
QY 179 GlyAlaGlyAspValHisSerValSerIleLysGlySerArgThrGlyTyrGlnSerMet 198

Db 564 GGTGCCGTGACGTCCACTCCGTCATATCAAGGTTTCGAGACCGGGTGCACCAACCATG 623
QY 199 SerArgAsnTyrGlyGlnAsnTyrGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSer 218
Db 624 TCAAGAACTGGGGCCAAACTGGCAAGTAAGTACTTACCTCAACGGCCAGCCCTGCC 683.
QY 219 PheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsn 238
Db 684 TT-AAGGTACCGCTAGCGACCGACGACCCCTGACTAG-CACACATTTGTTCTGCTCAT 741
QY 239 TrrGlnPheGlyGlnThrTyrGlnGlyProGlnPhe 250
Db 742 TGGCAATTGGGCGACACATTTGTGGTGGCAATTC 777

RESULT 14

BQ990398

LOCUS BQ990398 747 bp mRNA linear EST 21-AUG-2002

DEFINITION QGF20B04.Yg.ab1 QG EFGHJ lettuce serriola Lactuca sativa cDNA clone

ACCESSION QGF20B04, mRNA sequence.

VERSION BQ990398

KEYWORDS BQ990398.1 GI:22409933

SOURCE EST.

ORGANISM Lactuca sativa

REFERENCE Lactuca sativa

AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; campanulids; Asterales; Asteraceae; Cichorioideae;

Cichorieae; Lactuca.

1 (bases 1 to 747)

Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,

Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison

,P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,

Church,S., Jackson,L. and Bradford,K.

Lettuce and Sunflower ESTs from the Compositae Genome Project

http://comgenomics.ucdavis.edu/

Unpublished

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Fax: 1-(530)-752-9659

Email: akozik@veguc.org [michelmore@vegmail.ucdavis.edu]

belongs to contig QG_CA_Contig5532, see http://cgdb.ucdavis.edu/

for details.

Plate: QGF20 row: B column: 04.

FEATURES

source

1. 747

/organism="Lactuca sativa"

/mol_type="mRNA"

/cultivar="L.serriola"

/db_xref="taxon:4236"

/clone="QGF20B04"

/lab_host="E.coli"

/clone_lib="QG EFGHJ lettuce serriola"

/note="Vector: pBRCDNASfiAB; The library was constructed

from 10 different sources of RNA from a single genotype.

Separate cDNAs were generated using primers that

incorporated unique 5' and 3' tags to distinguish each

source of RNA. cDNAs were then pooled, size-fractionated,

directionally cloned into a custom medium-copy vector and

transformations made with four size classes to minimize

size bias. Details of each source of RNA and library

construction can be obtained at http://cgdb.ucdavis.edu/

TAG_SEQ=Not found"

BASE COUNT 215 a 149 c 172 g 211 t

ORIGIN

Alignment Scores:

Pred. No.: 3.97e-89 Length: 747

Score: 1060.00 Matches: 186

Percent Similarity: 93.90% Conservative: 14

Best Local Similarity: 87.32% Mismatches: 13.
 Query Match: 76.04% Indels: 0
 DB: 13 Gaps: 0

US-09-383-579c-10 (1-250) x BQ90398 (1-747)

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QY 38 G1G1YAspAlaSerGlyThrMetG1YG1YAlaCysG1YTrpG1YAsnLeuTrpSerGln 57
    |||
DB 32 GGGGGGATGCTCAGGAACAATGGGTGCTGCGGATATGGAATTTGATAGCCAA 91
QY 58 G1YTrpG1YThrAsnThrValAlaLeuSerThrAlaLeuPheAsnGlyLeuSerCys 77
    |||
DB 92 GGATATGATCAACAACACTGCGGCACTTAGCAGCTCTATCAATAATGTTGAGTTGT 151
QY 78 G1YAlaCysPheGluMetThrCysThrAsnAspProLysTrpCysLeuProGlyThrIle 97
    |||
DB 152 GGGCTCTGTTATGAGATGAGATGCAATGACGACCAAAATGGTGTCTCCCTGGTCCATA 211
QY 98 ArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnGlyGly 117
    |||
DB 212 ATGTACTGCAACCAATTTCTGTCCACCTAACCTGGCTGTCTTAACGATATGTTGGG 271
QY 118 TrpCysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAla 137
    |||
DB 272 TGGTGCACACCTCCCTCCCTCAACATTTTGACCTGGCTGAGCCTGCTTCTTCAAAATTTGCA 331
QY 138 GlnTrpArgAlaGlyIleValProValSerPheArgValProCysMetLysGly 157
    |||
DB 332 CAATATCGAGCTGGAATTTGACTGTCTGTCAATTTCAAGAGTCTTGTATGAGAAAGCA 391
QY 158 GlyValArgPheThrIleAsnGlyHisSerTrpPheAsnLeuValLeuIleThrAsnVal 177
    |||
DB 392 GGTGTAAGTTTAACTATAATGACCATTCAATTTCAACTGTTTGTATGATCAACGAT 451
QY 178 GlyGlyAlaGlyAspValHisSerValSerIleLysGlySerArgThrGlyTrpGlnSer 197
    |||
DB 452 GGAGGTGACGGGATGTCCACTCGGTATCAATCAAGGGTCAAAACCGGGTGGCAACCC 511
QY 198 MetSerArgAsnTrpGlyGlnAsnTrpGlnSerAsnTrpLeuAsnGlyGlnGlyLeu 217
    |||
DB 512 ATGTCAAGGAATGGGGGCAAAACTGGCAAGCAACTCAATCTTAACGGCAAAAGTCTT 571
QY 218 SerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSer 237
    |||
DB 572 TCTTTCAAGTCACAAACAAGTGAAGAAAGACATCAAGCTATAATGCGGACCATCA 631
QY 238 AsnTrpGlnPheGlyGlnThrTrpGlyGluGlyProGlnPhe 250
    |||
DB 632 AACTGGCAATTTGTCAGACATTTCAAGGGGCTCAATTT 670
  
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RESULT 15
 BU815493 685 bp mRNA linear EST 15-OCT-2002
 LOCUS NO42D11 Populus bark cDNA library Populus tremula x Populus
 DEFINITION tremuloides cDNA 5 prime, mRNA sequence.
 ACCESSION BU815493
 VERSION BU815493.1 GI:23974490
 KEYWORDS EST.
 SOURCE Populus tremula x Populus tremuloides
 ORGANISM Populus tremula x Populus tremuloides
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 1 (bases 1 to 685)
 REFERENCE Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
 AUTHORS The poplar tree transcriptome: Analysis of expressed sequence tags
 TITLE from multiple libraries
 JOURNAL Unpublished
 COMMENT Contact: BHALERAO RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279

Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.umu.se.
 Location/Qualifiers

FEATURES

source

1..685

/organism="Populus tremula x Populus tremuloides"

/mol_type="mRNA"

/db_xref="taxon:47664"

/issue_type="bark"

/clone_lib="Populus bark cDNA library"

BASE COUNT 155 a 172 c 180 g 178 t
 ORIGIN

Alignment Scores:

	4.49e-89	Length:	685
Pred. No.:	1059.00	Matches:	181
Score:	90.13%	Conservative:	20
Percent Similarity:	81.17%	Mismatches:	22
Best Local Similarity:	75.97%	Indels:	0
Query Match:	13	Gaps:	0

US-09-383-579c-10 (1-250) x BU815493 (1-685)

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QY 28 TrpGlnSerGlyHisAlaThrPheTrpGlyGlyGlyAspAlaSerGlyThrMetGlyGly 47
    |||
DB 3 TGGATTAATGCTCATGCAACATTTCTACGAGGTGGTGTGATGCTTCTGGCAATGGTGT 62
QY 48 AlaCysGlyTrpGlyAsnLeuTrpSerGlnGlyTrpGlyThrAsnThrValAlaLeuSer 67
    |||
DB 63 GCTTGGGTTATGGGAACCTTGTACAGCCAGGGTACGGTACTAATACTGACGCTTTAGC 122
QY 68 ThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGluMetThrCysThrAsn 87
    |||
DB 123 ACAGCTCTGTTCAACAGCGGGTTAAGCTGTGATCTTGTGAGATCAGGTGCGTGAAT 182
QY 88 AspProLysTrpCysLeuProGlyThrIleArgValThrAlaThrAsnPheCysProPro 107
    |||
DB 183 GACCCGAATGTGCTGCTGCTGCTCCATTGTGATCACCGCCACCAATTTCTGCCCTCCG 242
QY 108 AsnPheAlaLeuProAsnAsnAsnGlyGlyTrpCysAsnProProLeuGlnHisPheAsp 127
    |||
DB 243 AACATGCTCCTCAACATGACAGGGGCTGTGTAATCTCTCAACACCATTTTGAT 302
QY 128 MetAlaGluProAlaPheLeuGlnIleAlaGlnTrpArgAlaGlyIleValProValSer 147
    |||
DB 303 CTCTCCAGCTGTCTTCAACACATTTGCCAATATAGACAGGAATTTGCTGTGTCT 362
QY 148 PheArgArgValProCysMetLysLysGlyGlyValArgPheThrIleAsnGlyHisSer 167
    |||
DB 363 TACAGAGGGTACCTGCAAGAGAGAGAGCATTAAGTTCAAGTCAACGTCACCTCC 422
QY 168 TyrPheAsnLeuValLeuIleThrAsnValGlyGlyAlaGlyAspValHisSerValSer 187
    |||
DB 423 TACTTCAATCTAGTCTGATCACTAAGTGGCGGTGCTGATGATGATCTTCTGTGTCG 482
QY 188 IleLysGlySerArgThrGlyTrpGlnSerMetSerArgAsnTrpGlyGlnAsnTrpGln 207
    |||
DB 483 ATCAAGGGGTCCAGAGCTGTTGGCAGCAATGTCAAGGAAGTGGGGCAAAATTGGCAG 542
QY 208 SerAsnAsnTrpLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeuSerAspGlyArg 227
    |||
DB 543 AGCAACAATATCTCAATGGAACAAGTCTTCTTAAGTCAACCAAGTGTGATGTCGA 602
QY 228 ThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGlnPheGlyGlnThrTrpGlyGly 247
    |||
DB 603 ACCGTGCTCTCAATGTTGCTCTCTTAAGTGTGCTTGGGCAAGCTTCTCCGGC 662
QY 248 ProGlnPhe 250
    |||
DB 663 GCCCAGTTT 671
  
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Search completed: December 19, 2003, 01:02:44
 Job time : 2053 secs

